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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liaw, Chen W.  
Lu, Chin-Chun
- (ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 63
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Brown, Martin, Haller & McClain
  - (B) STREET: 1660 Union Street
  - (C) CITY: San Diego
  - (D) STATE: CA
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 92101-2926
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 29-SEPT-97
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/231,193
  - (B) FILING DATE: 20-APR-1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/052,449
  - (B) FILING DATE: 20-APR-1993
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 6362-9383C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619-238-0999
  - (B) TELEFAX: 619-238-0062

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4298 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

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(A) NAME/KEY: CDS  
(B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80 85	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160 165	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
190 195	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	

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205					210					215						
ATC Ile 220	ATC Ile 220	CTT Leu	TCT Ser	GCC Ala	AGC Ser	GAG Glu 225	GAC Asp	GAT Asp	GCT Ala	GCC Ala	ACT Thr 230	GTA Val	TAC Tyr	CGC Arg	GCA Ala	963
GCC Ala 235	GCG Ala	ATG Met	CTG Leu	AAC Asn	ATG Met 240	ACG Thr	GGC Gly	TCC Ser	GGG Gly	TAC Tyr 245	GTG Val	TGG Trp	CTG Leu	GTC Val	GGC Gly 250	1011
GAG Glu	CGC Arg	GAG Glu	ATC Ile	TCG Ser 255	GGG Gly	AAC Asn	GCC Ala	CTG Leu	CGC Arg 260	TAC Tyr	GCC Ala	CCA Pro	GAC Asp	GGC Gly 265	ATC Ile	1059
CTC Leu	GGG Gly	CTG Leu	CAG Gln 270	CTC Leu	ATC Ile	AAC Asn	GGC Gly	AAG Lys 275	AAC Asn	GAG Glu	TCG Ser	GCC Ala	CAC His 280	ATC Ile	AGC Ser	1107
GAC Asp	GCC Ala	GTG Val 285	GGC Gly	GTG Val	GTG Val	GCC Ala	CAG Gln 290	GCC Ala	GTG Val	CAC His	GAG Glu	CTC Leu 295	CTC Leu	GAG Glu	AAG Lys	1155
GAG Glu	AAC Asn 300	ATC Ile	ACC Thr	GAC Asp	CCG Pro	CCG Pro 305	CGG Arg	GGC Gly	TGC Cys	GTG Val	GGC Gly 310	AAC Asn	ACC Thr	AAC Asn	ATC Ile	1203
TGG Trp 315	AAG Lys	ACC Thr	GGG Gly	CCG Pro	CTC Leu 320	TTC Phe	AAG Lys	AGA Arg	GTG Val	CTG Leu 325	ATG Met	TCT Ser	TCC Ser	AAG Lys	TAT Tyr 330	1251
GCG Ala	GAT Asp	GGG Gly	GTG Val	ACT Thr 335	GGT Gly	CGC Arg	GTG Val	GAG Glu	TTC Phe 340	AAT Asn	GAG Glu	GAT Asp	GGG Gly	GAC Asp 345	CGG Arg	1299
AAG Lys	TTC Phe	GCC Ala	AAC Asn 350	TAC Tyr	AGC Ser	ATC Ile	ATG Met	AAC Asn 355	CTG Leu	CAG Gln	AAC Asn	CGC Arg	AAG Lys 360	CTG Leu	GTG Val	1347
CAA Gln	GTG Val	GGC Gly 365	ATC Ile	TAC Tyr	AAT Asn	GGC Gly	ACC Thr 370	CAC His	GTC Val	ATC Ile	CCT Pro	AAT Asn 375	GAC Asp	AGG Arg	AAG Lys	1395
ATC Ile 380	ATC Ile	TGG Trp	CCA Pro	GGC Gly	GGA Gly	GAG Glu 385	ACA Thr	GAG Glu	AAG Lys	CCT Pro	CGA Arg 390	GGG Gly	TAC Tyr	CAG Gln	ATG Met	1443
TCC Ser 395	ACC Thr	AGA Arg	CTG Leu	AAG Lys	ATT Ile 400	GTG Val	ACG Thr	ATC Ile	CAC His	CAG Gln 405	GAG Glu	CCC Pro	TTC Phe	GTG Val 410	TAC Tyr	1491
GTC Val	AAG Lys	CCC Pro	ACG Thr	CTG Leu 415	AGT Ser	GAT Asp	GGG Gly	ACA Thr	TGC Cys 420	AAG Lys	GAG Glu	GAG Glu	TTC Phe	ACA Thr 425	GTC Val	1539
AAC Asn	GGC Gly	GAC Asp	CCA Pro 430	GTC Val	AAG Lys	AAG Lys	GTG Val	ATC Ile 435	TGC Cys	ACC Thr	GGG Gly	CCC Pro	AAC Asn 440	GAC Asp	ACG Thr	1587
TCG Ser	CCG Pro	GGC Gly 445	AGC Ser	CCC Pro	CGC Arg	CAC His	ACG Thr 450	GTG Val	CCT Pro	CAG Gln	TGT Cys 455	TGC Cys	TAC Tyr	GGC Gly	TTT Phe	1635
TGC Cys	ATC Ile 460	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys 465	CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met 470	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	1683

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GAG Glu 475	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala 480	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly 485	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val 490	1731
AAC Asn	AAC Asn	AGC Ser	AAC Asn	AAG Lys 495	AAG Lys	GAG Glu	TGG Trp	AAT Asn	GGG Gly 500	ATG Met	ATG Met	GGC Gly	GAG Glu	CTG Leu 505	CTC Leu	1779
AGC Ser	GGG Gly	CAG Gln	GCA Ala 510	GAC Asp	ATG Met	ATC Ile	GTG Val	GCG Ala 515	CCG Pro	CTA Leu	ACC Thr	ATA Ile	AAC Asn	AAC Asn	GAG Glu	1827
CGC Arg	GCG Ala	CAG Gln 525	TAC Tyr	ATC Ile	GAG Glu	TTT Phe	TCC Ser 530	AAG Lys	CCC Pro	TTC Phe	AAG Lys	TAC Tyr 535	CAG Gln	GGC Gly	CTG Leu	1875
ACT Thr 540	ATT Ile	CTG Leu	GTC Val	AAG Lys	AAG Lys	GAG Glu 545	ATT Ile	CCC Pro	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp	TCG Ser	TTC Phe	1923
ATG Met 555	CAG Gln	CCG Pro	TTC Phe	CAG Gln	AGC Ser 560	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val 570	1971
CAC His	GTG Val	GTG Val	GCC Ala 575	GTG Val	ATG Met	CTG Leu	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg	TTC Phe	AGC Ser	CCC Pro 585	TTC Phe	2019
GGC Gly	CGG Arg	TTC Phe	AAG Lys 590	GTG Val	AAC Asn	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala 600	CTG Leu	ACC Thr		2067
CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met	TGG Trp	TTC Phe	TCC Ser 610	TGG Trp	GGC Gly	GTC Val	CTG Leu	CTC Leu	AAC Asn	TCC Ser	GGC Gly	2115
ATC Ile 620	GGG Gly	GAA Glu	GGC Gly	GCC Ala	CCC Pro	AGA Arg 625	AGC Ser	TTC Phe	TCA Ser	GCG Ala	CGC Arg 630	ATC Ile	CTG Leu	GGC Gly	ATG Met	2163
GTG Val 635	TGG Trp	GCC Ala	GGC Gly	TTT Phe	GCC Ala 640	ATG Met	ATC Ile	ATC Ile	GTG Val	GCC Ala 645	TCC Ser	TAC Tyr	ACC Thr	GCC Ala	AAC Asn 650	2211
CTG Leu	GCG Ala	GCC Ala	TTC Phe	CTG Leu 655	GTG Val	CTG Leu	GAC Asp	CGG Arg	CCG Pro	GAG Glu 660	GAG Glu	CGC Arg	ATC Ile	ACG Thr 665	GGC Gly	2259
ATC Ile	AAC Asn	GAC Asp	CCT Pro 670	CGG Arg	CTG Leu	AGG Arg	AAC Asn	CCC Pro 675	TCG Ser	GAC Asp	AAG Lys	TTT Phe 680	ATC Ile	TAC Tyr	GCC Ala	2307
ACG Thr	GTG Val	AAG Lys 685	CAG Gln	AGC Ser	TCC Ser	GTG Val	GAT Asp 690	ATC Ile	TAC Tyr	TTC Phe	CGG Arg	CGC Arg 695	CAG Gln	GTG Val	GAG Glu	2355
CTG Leu 700	AGC Ser	ACC Thr	ATG Met	TAC Tyr	CGG Arg	CAT His 705	ATG Met	GAG Glu	AAG Lys	CAC His	AAC Asn 710	TAC Tyr	GAG Glu	AGT Ser	GCG Ala	2403
GCG Ala 715	GAG Glu	GCC Ala	ATC Ile	CAG Gln	GCC Ala 720	GTG Val	AGA Arg	GAC Asp	AAC Asn	AAG Lys 725	CTG Leu	CAT His	GCC Ala	TTC Phe	ATC Ile 730	2451
TGG Trp	GAC Asp	TCG Ser	GCG Ala	GTG Val 735	CTG Leu	GAG Glu	TTC Phe	GAG Glu	GCC Ala 740	TCG Ser	CAG Gln	AAG Lys	TGC Cys	GAC Asp 745	CTG Leu	2499



GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TGC	GGC	TTC	GGC	ATA	GGC	ATG	2547	
Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met		
			750					755					760				
CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG	2595	
Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys		
			765				770					775					
TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG	2643	
Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg		
			780			785					790						
TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT	2691	
Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe		
					800					805					810		
GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	2739	
Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala		
				815					820					825			
GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	2787	
Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp		
			830					835					840				
GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	2835	
Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp		
			845				850					855					
CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	2883	
Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro		
						865					870						
AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	2931	
Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser		
					880					885					890		
TTC	AAG	AGG	CGT	AGG	TCC	TCC	AAA	GAC	ACG	AGC	ACC	GGG	GGT	GGA	CGC	2979	
Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg		
				895					900					905			
GGT	GCT	TTG	CAA	AAC	CAA	AAA	GAC	ACA	GTG	CTG	CCG	CGA	CGC	GCT	ATT	3027	
Gly	Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile		
			910					915					920				
GAG	AGG	GAG	GAG	GGC	CAG	CTG	CAG	CTG	TGT	TCC	CGT	CAT	AGG	GAG	AGC	3075	
Glu	Arg	Glu	Glu	Gly	Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser		
				925			930					935					
TGAGACTCCC			CGCCCGCCCT			CCTCTGCCCC			CTCCCCCGCA			GACAGACAGA			CAGACGGACG		3135
GGACAGCGGC			CCGGCCACG			CAGAGCCCCG			GAGCACCACG			GGGTCGGGGG			AGGAGCACCC		3195
CCAGCCTCCC			CCAGGCTGCG			CCTGCCCCGCC			CGCCGGTTGG			CCGGCTGGCC			GGTCCACCCC		3255
GTCCCGGCC			CGCGCGTGCC			CCCAGCGTGG			GGCTAACGGG			CGCCTTGTCT			GTGTATTTCT		3315
ATTTTGCAGC			AGTACCATCC			CACTGATATC			ACGGGCCCCG			TCAACCTCTC			AGATCCCTCG		3375
GTCAGCACCG			TGGTGTGAGG			CCCCCGGAGG			CGCCACCTG			CCCAGTTAGC			CCGGCCAAGG		3435
ACACTGATGG			GTCCTGCTGC			TCGGGAAGGC			CTGAGGGAAG			CCCACCCGCC			CCAGAGACTG		3495
CCCACCCTGG			GCCTCCCGTC			CGTCCGCCCG			CCCACCCCGC			TGCCTGGCGG			GCAGCCCCTG		3555
CTGGACCAAG			GTGCGGACCG			GAGCGGCTGA			GGACGGGGCA			GAGCTGAGTC			GGCTGGGCAG		3615
GGCCGCAGGG			CGCTCCGGCA			GAGGCAGGCC			CCTGGGGTCT			CTGAGCAGTG			GGGAGCGGGG		3675

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GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG	3735
CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTCGCC CCTCCTCGGG	3795
CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCCTC TTCTTGCGGC ACCGCCCACC	3855
AAACACCCCG TCTGCCCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC	3915
CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCCTC GGGCCGCCTC CTCCAGAATC	3975
GAGAGGGCTG AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG	4035
GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT GGGCACGGGA	4095
GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCCT GACCGGCCCC CCACCTTGTA	4155
CAGAACCAGC ACTCCCAGGG CCGAGCGCG TGCCTTCCCC GTGCGCAGCC GCGCTCTGCC	4215
CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG	4275
GTGATGCCTA AAGGAATGTC ACG	4298

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 938 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
			20					25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
		35				40					45				
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
	50					55					60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
	65				70				75					80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
				85					90					95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
		100					105						110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
	115					120						125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
	130					135					140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
145					150				155						160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
				165				170						175	

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Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
 180 185 190  
 Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
 195 200 205  
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
 210 215 220  
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
 225 230 235 240  
 Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly  
 245 250 255  
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
 260 265 270  
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
 275 280 285  
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
 290 295 300  
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
 305 310 315 320  
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
 325 330 335  
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
 340 345 350  
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
 355 360 365  
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
 370 375 380  
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
 385 390 395 400  
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
 405 410 415  
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
 420 425 430  
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
 435 440 445  
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
 450 455 460  
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
 465 470 475 480  
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
 485 490 495  
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met  
 500 505 510  
 Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu  
 515 520 525  
 Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys

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530		535		540
Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser				
545		550		555
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met				
		565		570
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn				
		580		585
				590
Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp				
		595		600
				605
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro				
		610		615
				620
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala				
		625		630
				635
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val				
		645		650
				655
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu				
		660		665
				670
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser				
		675		680
				685
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg				
		690		695
				700
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala				
		705		710
				715
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu				
		725		730
				735
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu				
		740		745
				750
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp				
		755		760
				765
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe				
		770		775
				780
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser				
		785		790
				795
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val				
		805		810
				815
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe				
		820		825
				830
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met				
		835		840
				845
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp				
		850		855
				860
Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe				
		865		870
				875
				880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser				

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	885		890		895										
Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln	Asn	Gln
			900					905					910		
Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu	Gly	Gln
		915					920					925			
Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser						
	930					935									

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 63 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..63

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	TCC	TAT	GAC	AAC	48
Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	
1				5				10						15		
AAG	CGC	GGA	CCC	AAG												63
Lys	Arg	Gly	Pro	Lys												
			20													

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn
1				5				10						15	
Lys	Arg	Gly	Pro	Lys											
			20												

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4068 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

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## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3899

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCTAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CCG GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806
Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	
195 200 205	
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC	854
Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	

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210					215					220						
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
		240				245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
		255			260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
		320				325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
		335			340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355				360						365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370				375						380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
		400				405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
					420					425					430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435				440						445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
				450				455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				
ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670

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Thr 480	Asn	Gly	Lys	His	Gly	Lys 485	Arg	Val	Arg	Gly	Val 490	Trp	Asn	Gly	Met	
ATT Ile 495	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr 500	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met 505	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu 510	1718
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu 515	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val 520	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro 525	TTT Phe	1766
GTG Val	GAG Glu	ACG Thr	GGC Gly 530	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val 535	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly 540	ACC Thr	GTC Val	1814
TCC Ser	CCC Pro	TCG Ser 545	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro 550	TAT Tyr	AGC Ser	CCT Pro	GCA Ala 555	GTG Val	TGG Trp	GTG Val	ATG Met	1862
ATG Met 560	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr 565	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr 570	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
GAG Glu 575	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val 580	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn 585	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys 590	1958
AAG Lys	TCC Ser	GGG Gly	GGC Gly	CCA Pro 595	GCT Ala	TTC Phe	ACT Thr	ATC Ile	GGC Gly 600	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu 605	CTG Leu	2006
TGG Trp	GCG Ala	CTG Leu 610	GTC Val	TTC Phe	AAC Asn	AAC Asn	TCA Ser	GTG Val 615	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro 620	CGG Arg	GGC Gly	2054
ACC Thr	ACC Thr	AGC Ser 625	AAG Lys	ATC Ile	ATG Met	GTT Val	CTG Leu 630	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe 635	GCT Ala	GTC Val	ATC Ile	2102
TTC Phe 640	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	ACG Thr	GCC Ala 645	AAC Asn	CTG Leu	GCC Ala	GCC Ala 650	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	2150
CAA Gln 655	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	GTG Val 660	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp 665	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg 670	2198
CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr 675	CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe 680	GGC Gly	ACG Thr	GTG Val	CCC Pro 685	AAC Asn	GGC Gly	2246
AGC Ser	ACG Thr	GAG Glu	CGG Arg	AAC Asn 690	ATC Ile	CGC Arg	AGT Ser	AAC Asn 695	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His 700	ACC Thr	CAC His	2294
ATG Met	GTC Val	AAG Lys 705	TTC Phe	AAC Asn	CAG Gln	CGC Arg	TCG Ser	GTG Val 710	GAG Glu	GAC Asp	GCG Ala	CTC Leu 715	ACC Thr	AGC Ser	CTC Leu	2342
AAG Lys 720	ATG Met	GGG Gly	AAG Lys	CTG Leu	GAT Asp	GCC Ala 725	TTC Phe	ATC Ile	TAT Tyr	GAT Asp	GCT Ala 730	GCT Ala	GTC Val	CTC Leu	AAC Asn	2390
TAC Tyr 735	ATG Met	GCA Ala	GGC Gly	AAG Lys	GAC Asp 740	GAG Glu	GGC Gly	TGC Cys	AAG Lys	CTG Leu 745	GTC Val	ACC Thr	ATT Ile	GGG Gly	TCT Ser 750	2438



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GGC Gly	AAG Lys	GTC Val	TTT Phe	GCT Ala	ACC Thr	ACT Thr	GBC Gly	TAC Tyr	GGC Gly	ATC Ile	GCC Ala	ATG Met	CAG Gln	AAG Lys	GAC Asp	2486
				755					760					765		
TCC Ser	CAC His	TGG Trp	AAG Lys	CGG Arg	GCC Ala	ATA Ile	GAC Asp	CTG Leu	GCG Ala	CTC Leu	TTG Leu	CAG Gln	TTC Phe	CTG Leu	GGG Gly	2534
			770					775					780			
GAC Asp	GGA Gly	GAG Glu	ACA Thr	CAG Gln	AAA Lys	CTG Leu	GAG Glu	ACA Thr	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly	ATC Ile	TGC Cys	2582
		785					790					795				
CAG Gln	AAT Asn	GAG Glu	AAG Lys	AAC Asn	GAG Glu	GTG Val	ATG Met	AGC Ser	AGC Ser	AAG Lys	CTG Leu	GAC Asp	ATC Ile	GAC Asp	AAC Asn	2630
	800					805					810					
ATG Met	GGA Gly	GGC Gly	GTC Val	TTC Phe	TAC Tyr	ATG Met	CTG Leu	CTG Leu	GTG Val	GCC Ala	ATG Met	GGG Gly	CTG Leu	GCC Ala	CTG Leu	2678
815					820					825					830	
CTG Leu	GTC Val	TTC Phe	GCC Ala	TGG Trp	GAG Glu	CAC His	CTG Leu	GTC Val	TAC Tyr	TGG Trp	AAG Lys	CTG Leu	CGC Arg	CAC His	TCG Ser	2726
				835					840					845		
GTG Val	CCC Pro	AAC Asn	TCA Ser	TCC Ser	CAG Gln	CTG Leu	GAC Asp	TTC Phe	CTG Leu	CTG Leu	GCT Ala	TTC Phe	AGC Ser	AGG Arg	GGC Gly	2774
			850					855					860			
ATC Ile	TAC Tyr	AGC Ser	TGC Cys	TTC Phe	AGC Ser	GGG Gly	GTG Val	CAG Gln	AGC Ser	CTC Leu	GCC Ala	AGC Ser	CCA Pro	CCG Pro	CGG Arg	2822
		865					870					875				
CAG Gln	GCC Ala	AGC Ser	CCG Pro	GAC Asp	CTC Leu	ACG Thr	GCC Ala	AGC Ser	TCG Ser	GCC Ala	CAG Gln	GCC Ala	AGC Ser	GTG Val	CTC Leu	2870
	880					885					890					
AAG Lys	ATT Ile	CTG Leu	CAG Gln	GCA Ala	GCC Ala	CGC Arg	GAC Asp	ATG Met	GTG Val	ACC Thr	ACG Thr	GCG Ala	GGC Gly	GTA Val	AGC Ser	2918
895					900					905					910	
AAC Asn	TCC Ser	CTG Leu	GAC Asp	CGC Arg	GCC Ala	ACT Thr	CGC Arg	ACC Thr	ATC Ile	GAG Glu	AAT Asn	TGG Trp	GGT Gly	GGC Gly	GGC Gly	2966
				915				920						925		
CGC Arg	CGT Arg	GCG Ala	CCC Pro	CCA Pro	CCG Pro	TCC Ser	CCC Pro	TGC Cys	CCG Pro	ACC Thr	CCG Pro	CGG Arg	TCT Ser	GGC Gly	CCC Pro	3014
			930					935					940			
AGC Ser	CCA Pro	TGC Cys	CTG Leu	CCC Pro	ACC Thr	CCC Pro	GAC Asp	CCG Pro	CCC Pro	CCA Pro	GAG Glu	CCG Pro	AGC Ser	CCC Pro	ACG Thr	3062
		945					950					955				
GGC Gly	TGG Trp	GGA Gly	CCG Pro	CCA Pro	GAC Asp	GGG Gly	GGT Gly	CGC Arg	GCG Ala	GCG Ala	CTT Leu	GTG Val	CGC Arg	AGG Arg	GCT Ala	3110
	960					965					970					
CCG Pro	CAG Gln	CCC Pro	CCG Pro	GGC Gly	CGC Arg	CCC Pro	CCG Pro	ACG Thr	CCG Pro	GGG Gly	CCG Pro	CCC Pro	CTG Leu	TCC Ser	GAC Asp	3158
	975				980					985					990	
GTC Val	TCC Ser	CGA Arg	GTG Val	TCG Ser	CGC Arg	CGC Arg	CCA Pro	GCC Ala	TGG Trp	GAG Glu	GCG Ala	CGG Arg	TGG Trp	CCG Pro	GTG Val	3206
				995					1000						1005	
CGG Arg	ACC Thr	GGG Gly	CAC His	TGC Cys	GGG Gly	AGG Arg	CAC His	CTC Leu	TCG Ser	GCC Ala	TCC Ser	GAG Glu	CGG Arg	CCC Pro	CTG Leu	3254
			1010					1015					1020			

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TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
AAC GCG GCC TGG GCC CCG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GGC GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG	3986
GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA	4046
TCAGTGACCT CAGCTAGCCT CA	4068

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1236 amino acids

Met 1	Gly	Gly	Ala	Leu 5	Gly	Pro	Ala	Leu 10	Leu	Thr	Ser	Leu	Phe 15	Gly	
Ala	Trp	Ala	Gly 20	Leu	Gly	Pro	Gly	Gln 25	Gly	Glu	Gln	Gly	Met 30	Thr	Val
Ala	Val	Val 35	Phe	Ser	Ser	Ser	Gly 40	Pro	Pro	Gln	Ala	Gln 45	Phe	Arg	Val
Arg	Leu 50	Thr	Pro	Gln	Ser	Phe 55	Leu	Asp	Leu	Pro	Leu 60	Glu	Ile	Gln	Pro
Leu 65	Thr	Val	Gly	Val	Asn 70	Thr	Thr	Asn	Pro	Ser 75	Ser	Leu	Leu	Thr	Gln 80
Ile	Cys	Gly	Leu	Leu 85	Gly	Ala	Ala	His 90	Val	His	Gly	Ile	Val	Phe 95	Glu
Asp	Asn	Val	Asp 100	Thr	Glu	Ala	Val	Ala 105	Gln	Ile	Leu	Asp	Phe 110	Ile	Ser
Ser	Gln	Thr 115	His	Val	Pro	Ile	Leu 120	Ser	Ile	Ser	Gly	Gly 125	Ser	Ala	Val
Val	Leu 130	Thr	Pro	Lys	Glu	Pro 135	Gly	Ser	Ala	Phe	Leu 140	Gln	Leu	Gly	Val
Ser 145	Leu	Glu	Gln	Gln	Leu 150	Gln	Val	Leu	Phe	Lys 155	Val	Leu	Glu	Glu	Tyr 160
Asp	Trp	Ser	Ala	Phe 165	Ala	Val	Ile	Thr	Ser 170	Leu	His	Pro	Gly	His 175	Ala
Leu	Phe	Leu	Glu 180	Gly	Val	Arg	Ala	Val 185	Ala	Asp	Ala	Ser	His 190	Val	Ser
Trp	Arg	Leu 195	Leu	Asp	Val	Val	Thr 200	Leu	Glu	Leu	Asp	Pro 205	Gly	Gly	Pro
Arg	Ala 210	Arg	Thr	Gln	Arg	Leu 215	Leu	Arg	Gln	Leu	Asp 220	Ala	Pro	Val	Phe
Val 225	Ala	Tyr	Cys	Ser	Arg 230	Glu	Glu	Ala	Glu	Val 235	Leu	Phe	Ala	Glu	Ala 240
Ala	Gln	Ala	Gly	Leu 245	Val	Gly	Pro	Gly	His 250	Val	Trp	Leu	Val	Pro 255	Asn
Leu	Ala	Leu	Gly 260	Ser	Thr	Asp	Ala	Pro 265	Pro	Ala	Thr	Phe	Pro 270	Val	Gly
Leu	Ile	Ser 275	Val	Val	Thr	Glu	Ser 280	Trp	Arg	Leu	Ser	Leu 285	Arg	Gln	Lys
Val	Arg 290	Asp	Gly	Val	Ala	Ile 295	Leu	Ala	Leu	Gly	Ala 300	His	Ser	Tyr	Trp
Arg 305	Gln	His	Gly	Thr	Leu 310	Pro	Ala	Pro	Ala	Gly 315	Asp	Cys	Arg	Val	His 320

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Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu
				325					330					335	
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr
			340					345					350		
Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu
		355					360					365			
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr
	370					375					380				
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser
385					390					395					400
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val
				405					410					415	
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro
			420					425					430		
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro
		435					440					445			
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys
	450					455					460				
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn
465					470				475						480
Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly
				485					490					495	
Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile
			500					505					510		
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu
		515					520					525			
Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro
	530					535					540				
Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe
545					550					555					560
Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr
				565					570					575	
Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser
			580					585					590		
Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala
		595					600					605			
Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr
	610					615					620				
Ser	Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu
625					630					635					640
Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr
				645					650					655	
Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln
			660					665					670		

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Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr
		675					680					685			
Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val
	690					695					700				
Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met
705					710					715					720
Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met
				725					730					735	
Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys
			740					745					750		
Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His
		755					760					765			
Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly
	770					775					780				
Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn
785					790					795					800
Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly
				805					810					815	
Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val
			820					825					830		
Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro
			835				840					845			
Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr
	850					855					860				
Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala
865					870					875					880
Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile
				885					890					895	
Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser
			900					905					910		
Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg
		915					920					925			
Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro
						935					940				
Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp
945					950					955					960
Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln
				965					970					975	
Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser
			980					985					990		
Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr
		995					1000					1005			
Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro
	1010					1015					1020				

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Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg  
 1025 1030 1035 1040

Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro  
 1045 1050 1055

Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala  
 1060 1065 1070

Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser  
 1075 1080 1085

Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr  
 1090 1095 1100

Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu  
 1105 1110 1115 1120

Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln  
 1125 1130 1135

Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val  
 1140 1145 1150

Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys  
 1155 1160 1165

Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala  
 1170 1175 1180

Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly  
 1185 1190 1195 1200

Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly  
 1205 1210 1215

Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu  
 1220 1225 1230

Glu Ser Glu Val  
 1235

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG  
 Ser Glu Ala Gln Pro Val Pro  
 1 5

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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 7 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro  
 1 5

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G

11

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4808 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCCC CGTGGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGGC CGCAGCATGC GGGAACCCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300
AGTGGCGACT ATG GGC AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG	349
Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro	
1 5 10	
GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG	397
Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys	
15 20 25	
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC	445

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Gly 30	Pro	Pro	Ala	Leu	Asn 35	Ile	Ala	Val	Met	Leu 40	Gly	His	Ser	His	Asp 45	
GTG	ACA	GAG	CGC	GAA	CTT	CGA	ACA	CTG	TGG	GGC	CCC	GAG	CAG	GCG	GCG	493
Val	Thr	Glu	Arg	Glu 50	Leu	Arg	Thr	Leu	Trp 55	Gly	Pro	Glu	Gln	Ala	Ala	
GGG	CTG	CCC	CTG	GAC	GTG	AAC	GTG	GTA	GCT	CTG	CTG	ATG	AAC	CGC	ACC	541
Gly	Leu	Pro	Leu	Asp 65	Val	Asn	Val	Val 70	Ala	Leu	Leu	Met	Asn 75	Arg	Thr	
GAC	CCC	AAG	AGC	CTC	ATC	ACG	CAC	GTG	TGC	GAC	CTC	ATG	TCC	GGG	GCA	589
Asp	Pro	Lys 80	Ser	Leu	Ile	Thr	His 85	Val	Cys	Asp	Leu	Met 90	Ser	Gly	Ala	
CGC	ATC	CAC	GGC	CTC	GTG	TTT	GGG	GAC	GAC	ACG	GAC	CAG	GAG	GCC	GTA	637
Arg	Ile 95	His	Gly	Leu	Val	Phe 100	Gly	Asp	Asp	Thr	Asp 105	Gln	Glu	Ala	Val	
GCC	CAG	ATG	CTG	GAT	TTT	ATC	TCC	TCC	CAC	ACC	TTC	GTC	CCC	ATC	TTG	685
Ala	Gln	Met	Leu	Asp 110	Phe 115	Ile	Ser	Ser	His	Thr 120	Phe	Val	Pro	Ile	Leu 125	
GGC	ATT	CAT	GGG	GGC	GCA	TCT	ATG	ATC	ATG	GCT	GAC	AAG	GAT	CCG	ACG	733
Gly	Ile	His	Gly	Gly 130	Ala	Ser	Met	Ile	Met 135	Ala	Asp	Lys	Asp	Pro	Thr	
TCT	ACC	TTC	TTC	CAG	TTT	GGA	GCG	TCC	ATC	CAG	CAG	CAA	GCC	ACG	GTC	781
Ser	Thr	Phe	Phe 145	Gln	Phe	Gly	Ala	Ser 150	Ile	Gln	Gln	Gln	Ala 155	Thr	Val	
ATG	CTG	AAG	ATC	ATG	CAG	GAT	TAT	GAC	TGG	CAT	GTC	TTC	TCC	CTG	GTG	829
Met	Leu	Lys 160	Ile	Met	Gln	Asp	Tyr 165	Asp	Trp	His	Val	Phe 170	Ser	Leu	Val	
ACC	ACT	ATC	TTC	CCT	GGC	TAC	AGG	GAA	TTC	ATC	AGC	TTC	GTC	AAG	ACC	877
Thr	Thr	Ile	Phe	Pro	Gly	Tyr 180	Arg	Glu	Phe	Ile	Ser 185	Phe	Val	Lys	Thr	
ACA	GTG	GAC	AAC	AGC	TTT	GTG	GGC	TGG	GAC	ATG	CAG	AAT	GTG	ATC	ACA	925
Thr	Val	Asp	Asn	Ser	Phe 195	Val	Gly	Trp	Asp	Met 200	Gln	Asn	Val	Ile	Thr 205	
CTG	GAC	ACT	TCC	TTT	GAG	GAT	GCA	AAG	ACA	CAA	GTC	CAG	CTG	AAG	AAG	973
Leu	Asp	Thr	Ser	Phe 210	Glu	Asp	Ala	Lys 215	Thr	Gln	Val	Gln	Leu	Lys 220	Lys	
ATC	CAC	TCT	TCT	GTC	ATC	TTG	CTC	TAC	TGT	TCC	AAA	GAC	GAG	GCT	GTT	1021
Ile	His	Ser	Ser 225	Val	Ile	Leu	Leu	Tyr 230	Cys	Ser	Lys	Asp	Glu 235	Ala	Val	
CTC	ATT	CTG	AGT	GAG	GCC	CGC	TCC	CTT	GGC	CTC	ACC	GGG	TAT	GAT	TTC	1069
Leu	Ile	Leu	Ser	Glu	Ala	Arg	Ser 245	Leu	Gly	Leu	Thr	Gly 250	Tyr	Asp	Phe	
TTC	TGG	ATT	GTC	CCC	AGC	TTG	GTC	TCT	GGG	AAC	ACG	GAG	CTC	ATC	CCA	1117
Phe	Trp	Ile	Val	Pro	Ser	Leu 260	Val	Ser	Gly	Asn 265	Thr	Glu	Leu	Ile	Pro	
AAA	GAG	TTT	CCA	TCG	GGA	CTC	ATT	TCT	GTC	TCC	TAC	GAT	GAC	TGG	GAC	1165
Lys	Glu	Phe	Pro	Ser	Gly 275	Leu	Ile	Ser	Val	Ser 280	Tyr	Asp	Asp	Trp	Asp 285	
TAC	AGC	CTG	GAG	GCG	AGA	GTG	AGG	GAC	GGC	ATT	GGC	ATC	CTA	ACC	ACC	1213
Tyr	Ser	Leu	Glu	Ala 290	Arg	Val	Arg	Asp	Gly 295	Ile	Gly	Ile	Leu	Thr 300	Thr	



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GCT	GCA	TCT	TCT	ATG	CTG	GAG	AAG	TTC	TCC	TAC	ATC	CCC	GAG	GCC	AAG	1261
Ala	Ala	Ser	Ser	Met	Leu	Glu	Lys	Phe	Ser	Tyr	Ile	Pro	Glu	Ala	Lys	
			305					310					315			
GCC	AGC	TGC	TAC	GGG	CAG	ATG	GAG	AGG	CCA	GAG	GTC	CCG	ATG	CAC	ACC	1309
Ala	Ser	Cys	Tyr	Gly	Gln	Met	Glu	Arg	Pro	Glu	Val	Pro	Met	His	Thr	
		320					325					330				
TTG	CAC	CCA	TTT	ATG	GTC	AAT	GTT	ACA	TGG	GAT	GGC	AAA	GAC	TTA	TCC	1357
Leu	His	Pro	Phe	Met	Val	Asn	Val	Thr	Trp	Asp	Gly	Lys	Asp	Leu	Ser	
	335					340					345					
TTC	ACT	GAG	GAA	GGC	TAC	CAG	GTG	CAC	CCC	AGG	CTG	GTG	GTG	ATT	GTG	1405
Phe	Thr	Glu	Glu	Gly	Tyr	Gln	Val	His	Pro	Arg	Leu	Val	Val	Ile	Val	
350					355					360					365	
CTG	AAC	AAA	GAC	CGG	GAA	TGG	GAA	AAG	GTG	GGC	AAG	TGG	GAG	AAC	CAT	1453
Leu	Asn	Lys	Asp	Arg	Glu	Trp	Glu	Lys	Val	Gly	Lys	Trp	Glu	Asn	His	
				370					375					380		
ACG	CTG	AGC	CTG	AGG	CAC	GCC	GTG	TGG	CCC	AGG	TAC	AAG	TCC	TTC	TCC	1501
Thr	Leu	Ser	Leu	Arg	His	Ala	Val	Trp	Pro	Arg	Tyr	Lys	Ser	Phe	Ser	
			385					390					395			
GAC	TGT	GAG	CCG	GAT	GAC	AAC	CAT	CTC	AGC	ATC	GTC	ACC	CTG	GAG	GAG	1549
Asp	Cys	Glu	Pro	Asp	Asp	Asn	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	
		400					405					410				
GCC	CCA	TTC	GTC	ATC	GTG	GAA	GAC	ATA	GAC	CCC	CTG	ACC	GAG	ACG	TGT	1597
Ala	Pro	Phe	Val	Ile	Val	Glu	Asp	Ile	Asp	Pro	Leu	Thr	Glu	Thr	Cys	
	415					420					425					
GTG	AGG	AAC	ACC	GTG	CCA	TGT	CGG	AAG	TTC	GTC	AAA	ATC	AAC	AAT	TCA	1645
Val	Arg	Asn	Thr	Val	Pro	Cys	Arg	Lys	Phe	Val	Lys	Ile	Asn	Asn	Ser	
430					435					440					445	
ACC	AAT	GAG	GGG	ATG	AAT	GTG	AAG	AAA	TGC	TGC	AAG	GGG	TTC	TGC	ATT	1693
Thr	Asn	Glu	Gly	Met	Asn	Val	Lys	Lys	Cys	Cys	Lys	Gly	Phe	Cys	Ile	
				450					455					460		
GAT	ATT	CTG	AAG	AAG	CTT	TCC	AGA	ACT	GTG	AAG	TTT	ACT	TAC	GAC	CTC	1741
Asp	Ile	Leu	Lys	Lys	Leu	Ser	Arg	Thr	Val	Lys	Phe	Thr	Tyr	Asp	Leu	
			465					470					475			
TAT	CTG	GTG	ACC	AAT	GGG	AAG	CAT	GGC	AAG	AAA	GTT	AAC	AAT	GTG	TGG	1789
Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Lys	Val	Asn	Asn	Val	Trp	
	480						485					490				
AAT	GGA	ATG	ATC	GGT	GAA	GTG	GTC	TAT	CAA	CGG	GCA	GTC	ATG	GCA	GTT	1837
Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Tyr	Gln	Arg	Ala	Val	Met	Ala	Val	
	495					500					505					
GGC	TCG	CTC	ACC	ATC	AAT	GAG	GAA	CGT	TCT	GAA	GTG	GTG	GAC	TTC	TCT	1885
Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Val	Val	Asp	Phe	Ser	
510					515					520					525	
GTG	CCC	TTT	GTG	GAA	ACG	GGA	ATC	AGT	GTC	ATG	GTT	TCA	AGA	AGT	AAT	1933
Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ser	Arg	Ser	Asn	
				530					535					540		
GGC	ACC	GTC	TCA	CCT	TCT	GCT	TTT	CTA	GAA	CCA	TTC	AGC	GCC	TCT	GTC	1981
Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Ser	Val	
			545					550					555			
TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATT	GTT	TCT	GCC	ATA	GCT	GTT	2029
Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Ile	Ala	Val	
		560					565					570				

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TGG	GTC	TTG	GAT	TAC	TCC	AGC	CCT	GTT	GGA	TAC	AAC	AGA	AAC	TTA	GCC	2077
Trp	Val	Leu	Asp	Tyr	Ser	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Asn	Leu	Ala	
	575					580					585					
AAA	GGG	AAA	GCA	CCC	CAT	GGG	CCT	TCT	TTT	ACA	ATT	GGA	AAA	GCT	ATA	2125
Lys	Gly	Lys	Ala	Pro	His	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	
590					595					600					605	
TGG	CTT	CTT	TGG	GGC	CTG	GTG	TTC	AAT	AAC	TCC	GTG	CCT	GTC	CAG	AAT	2173
Trp	Leu	Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	
				610					615					620		
CCT	AAA	GGG	ACC	ACC	AGC	AAG	ATC	ATG	GTA	TCT	GTA	TGG	GCC	TTC	TTC	2221
Pro	Lys	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	
			625					630					635			
GCT	GTC	ATA	TTC	CTG	GCT	AGC	TAC	ACA	GCC	AAT	CTG	GCT	GCC	TTC	ATG	2269
Ala	Val	Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	
		640					645					650				
ATC	CAA	GAG	GAA	TTT	GTG	GAC	CAA	GTG	ACC	GGC	CTC	AGT	GAC	AAA	AAG	2317
Ile	Gln	Glu	Glu	Phe	Val	Asp	Gln	Val	Thr	Gly	Leu	Ser	Asp	Lys	Lys	
	655					660					665					
TTT	CAG	AGA	CCT	CAT	GAC	TAT	TCC	CCA	CCT	TTT	CGA	TTT	GGG	ACA	GTG	2365
Phe	Gln	Arg	Pro	His	Asp	Tyr	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	
670					675					680					685	
CCT	AAT	GGA	AGC	ACG	GAG	AGA	AAC	ATT	CGG	AAT	AAC	TAT	CCC	TAC	ATG	2413
Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Pro	Tyr	Met	
				690					695					700		
CAT	CAG	TAC	ATG	ACC	AAA	TTT	AAT	CAG	AAA	GGA	GTA	GAG	GAC	GCC	TTG	2461
His	Gln	Tyr	Met	Thr	Lys	Phe	Asn	Gln	Lys	Gly	Val	Glu	Asp	Ala	Leu	
			705					710					715			
GTC	AGC	CTG	AAA	ACG	GGG	AAG	CTG	GAC	GCT	TTC	ATC	TAC	GAT	GCC	GCA	2509
Val	Ser	Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
		720					725					730				
GTC	TTG	AAT	TAC	AAG	GCT	GGG	AGG	GAT	GAA	GGC	TGC	AAG	CTG	GTG	ACC	2557
Val	Leu	Asn	Tyr	Lys	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
	735					740					745					
ATC	GGG	AGT	GGG	TAC	ATC	TTT	GCC	ACC	ACC	GGT	TAT	GGA	ATT	GCC	CTT	2605
Ile	Gly	Ser	Gly	Tyr	Ile	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	
750					755					760					765	
CAG	AAA	GGC	TCT	CCT	TGG	AAG	AGG	CAG	ATC	GAC	CTG	GCC	TTG	CTT	CAG	2653
Gln	Lys	Gly	Ser	Pro	Trp	Lys	Arg	Gln	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
				770					775					780		
TTT	GTG	GGT	GAT	GGT	GAG	ATG	GAG	GAG	CTG	GAG	ACC	CTG	TGG	CTC	ACT	2701
Phe	Val	Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Thr	Leu	Trp	Leu	Thr	
			785					790					795			
GGG	ATC	TGC	CAC	AAC	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	CAG	CTG	GAC	2749
Gly	Ile	Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	
		800					805					810				
ATT	GAC	AAC	ATG	GCG	GGC	GTA	TTC	TAC	ATG	CTG	GCT	GCC	GCC	ATG	GCC	2797
Ile	Asp	Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Ala	Ala	Ala	Met	Ala	
	815					820					825					
CTT	AGC	CTC	ATC	ACC	TTC	ATC	TGG	GAG	CAC	CTC	TTC	TAC	TGG	AAG	CTG	2845
Leu	Ser	Leu	Ile	Thr	Phe	Ile	Trp	Glu	His	Leu	Phe	Tyr	Trp	Lys	Leu	
830					835					840					845	

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CGC	TTC	TGT	TTC	ACG	GGC	GTG	TGC	TCC	GAC	CGG	CCT	GGG	TTG	CTC	TTC	2893
Arg	Phe	Cys	Phe	Thr	Gly	Val	Cys	Ser	Asp	Arg	Pro	Gly	Leu	Leu	Phe	
				850					855					860		
TCC	ATC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	ATT	CAT	GGA	GTG	CAC	ATT	GAA	2941
Ser	Ile	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	His	Ile	Glu	
			865					870					875			
GAA	AAG	AAG	AAG	TCT	CCA	GAC	TTC	AAT	CTG	ACG	GGA	TCC	CAG	AGC	AAC	2989
Glu	Lys	Lys	Lys	Ser	Pro	Asp	Phe	Asn	Leu	Thr	Gly	Ser	Gln	Ser	Asn	
			880				885					890				
ATG	TTA	AAA	CTC	CTC	CGG	TCA	GCC	AAA	AAC	ATT	TCC	AGC	ATG	TCC	AAC	3037
Met	Leu	Lys	Leu	Leu	Arg	Ser	Ala	Lys	Asn	Ile	Ser	Ser	Met	Ser	Asn	
	895					900					905					
ATG	AAC	TCC	TCA	AGA	ATG	GAC	TCA	CCC	AAA	AGA	GCT	GCT	GAC	TTC	ATC	3085
Met	Asn	Ser	Ser	Arg	Met	Asp	Ser	Pro	Lys	Arg	Ala	Ala	Asp	Phe	Ile	
	910				915					920					925	
CAA	AGA	GGT	TCC	CTC	ATC	ATG	GAC	ATG	GTT	TCA	GAT	AAG	GGG	AAT	TTG	3133
Gln	Arg	Gly	Ser	Leu	Ile	Met	Asp	Met	Val	Ser	Asp	Lys	Gly	Asn	Leu	
				930					935					940		
ATG	TAC	TCA	GAC	AAC	AGG	TCC	TTT	CAG	GGG	AAA	GAG	AGC	ATT	TTT	GGA	3181
Met	Tyr	Ser	Asp	Asn	Arg	Ser	Phe	Gln	Gly	Lys	Glu	Ser	Ile	Phe	Gly	
			945					950					955			
GAC	AAC	ATG	AAC	GAA	CTC	CAA	ACA	TTT	GTG	GCC	AAC	CGG	CAG	AAG	GAT	3229
Asp	Asn	Met	Asn	Glu	Leu	Gln	Thr	Phe	Val	Ala	Asn	Arg	Gln	Lys	Asp	
		960					965					970				
AAC	CTC	AAT	AAC	TAT	GTA	TTC	CAG	GGA	CAA	CAT	CCT	CTT	ACT	CTC	AAT	3277
Asn	Leu	Asn	Asn	Tyr	Val	Phe	Gln	Gly	Gln	His	Pro	Leu	Thr	Leu	Asn	
	975					980					985					
GAG	TCC	AAC	CCT	AAC	ACG	GTG	GAG	GTG	GCC	GTG	AGC	ACA	GAA	TCC	AAA	3325
Glu	Ser	Asn	Pro	Asn	Thr	Val	Glu	Val	Ala	Val	Ser	Thr	Glu	Ser	Lys	
	990				995					1000					1005	
GCG	AAC	TCT	AGA	CCC	CGG	CAG	CTG	TGG	AAG	AAA	TCC	GTG	GAT	TCC	ATA	3373
Ala	Asn	Ser	Arg	Pro	Arg	Gln	Leu	Trp	Lys	Lys	Ser	Val	Asp	Ser	Ile	
				1010					1015					1020		
CGC	CAG	GAT	TCA	CTA	TCC	CAG	AAT	CCA	GTC	TCC	CAG	AGG	GAT	GAG	GCA	3421
Arg	Gln	Asp	Ser	Leu	Ser	Gln	Asn	Pro	Val	Ser	Gln	Arg	Asp	Glu	Ala	
			1025					1030					1035			
ACA	GCA	GAG	AAT	AGG	ACC	CAC	TCC	CTA	AAG	AGC	CCT	AGG	TAT	CTT	CCA	3469
Thr	Ala	Glu	Asn	Arg	Thr	His	Ser	Leu	Lys	Ser	Pro	Arg	Tyr	Leu	Pro	
			1040				1045					1050				
GAA	GAG	ATG	GCC	CAC	TCT	GAC	ATT	TCA	GAA	ACG	TCA	AAT	CGG	GCC	ACG	3517
Glu	Glu	Met	Ala	His	Ser	Asp	Ile	Ser	Glu	Thr	Ser	Asn	Arg	Ala	Thr	
	1055					1060					1065					
TGC	CAC	AGG	GAA	CCT	GAC	AAC	AGT	AAG	AAC	CAC	AAA	ACC	AAG	GAC	AAC	3565
Cys	His	Arg	Glu	Pro	Asp	Asn	Ser	Lys	Asn	His	Lys	Thr	Lys	Asp	Asn	
	1070				1075					1080					1085	
TTT	AAA	AGG	TCA	GTG	GCC	TCC	AAA	TAC	CCC	AAG	GAC	TGT	AGT	GAG	GTC	3613
Phe	Lys	Arg	Ser	Val	Ala	Ser	Lys	Tyr	Pro	Lys	Asp	Cys	Ser	Glu	Val	
				1090					1095					1100		
GAG	CGC	ACC	TAC	CTG	AAA	ACC	AAA	TCA	AGC	TCC	CCT	AGA	GAC	AAG	ATC	3661
Glu	Arg	Thr	Tyr	Leu	Lys	Thr	Lys	Ser	Ser	Ser	Pro	Arg	Asp	Lys	Ile	
			1105					1110					1115			

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TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Glu Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381
TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477

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TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG	4525
Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu	
1390 1395 1400 1405	
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT	4573
Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp	
1410 1415 1420	
GTG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT	4621
Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn	
1425 1430 1435	
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG	4669
Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val	
1440 1445 1450	
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT	4722
Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val	
1455 1460 146	
TTTATCTATA GGGAAATACA CGTAATGGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC	4782
AATAGTGCCC TGCTAAGAGG AAGGAG	4808

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1464 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu	
1 5 10 15	
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro	
20 25 30	
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu	
35 40 45	
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro	
50 55 60	
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys	
65 70 75 80	
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His	
85 90 95	
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met	
100 105 110	
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His	
115 120 125	
Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe	
130 135 140	
Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val Met Leu Lys	
145 150 155 160	
Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile	

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165										170					175						
Phe	Pro	Gly	Tyr	Arg	Glu	Phe	Ile	Ser	Phe	Val	Lys	Thr	Thr	Val	Asp						
			180					185						190							
Asn	Ser	Phe	Val	Gly	Trp	Asp	Met	Gln	Asn	Val	Ile	Thr	Leu	Asp	Thr						
		195					200					205									
Ser	Phe	Glu	Asp	Ala	Lys	Thr	Gln	Val	Gln	Leu	Lys	Lys	Ile	His	Ser						
	210					215					220										
Ser	Val	Ile	Leu	Leu	Tyr	Cys	Ser	Lys	Asp	Glu	Ala	Val	Leu	Ile	Leu						
	225				230					235					240						
Ser	Glu	Ala	Arg	Ser	Leu	Gly	Leu	Thr	Gly	Tyr	Asp	Phe	Phe	Trp	Ile						
				245					250					255							
Val	Pro	Ser	Leu	Val	Ser	Gly	Asn	Thr	Glu	Leu	Ile	Pro	Lys	Glu	Phe						
			260					265					270								
Pro	Ser	Gly	Leu	Ile	Ser	Val	Ser	Tyr	Asp	Asp	Trp	Asp	Tyr	Ser	Leu						
		275					280					285									
Glu	Ala	Arg	Val	Arg	Asp	Gly	Ile	Gly	Ile	Leu	Thr	Thr	Ala	Ala	Ser						
	290					295					300										
Ser	Met	Leu	Glu	Lys	Phe	Ser	Tyr	Ile	Pro	Glu	Ala	Lys	Ala	Ser	Cys						
	305				310					315				320							
Tyr	Gly	Gln	Met	Glu	Arg	Pro	Glu	Val	Pro	Met	His	Thr	Leu	His	Pro						
				325					330					335							
Phe	Met	Val	Asn	Val	Thr	Trp	Asp	Gly	Lys	Asp	Leu	Ser	Phe	Thr	Glu						
			340					345					350								
Glu	Gly	Tyr	Gln	Val	His	Pro	Arg	Leu	Val	Val	Ile	Val	Leu	Asn	Lys						
		355					360					365									
Asp	Arg	Glu	Trp	Glu	Lys	Val	Gly	Lys	Trp	Glu	Asn	His	Thr	Leu	Ser						
	370					375					380										
Leu	Arg	His	Ala	Val	Trp	Pro	Arg	Tyr	Lys	Ser	Phe	Ser	Asp	Cys	Glu						
	385				390				395					400							
Pro	Asp	Asp	Asn	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe						
			405						410					415							
Val	Ile	Val	Glu	Asp	Ile	Asp	Pro	Leu	Thr	Glu	Thr	Cys	Val	Arg	Asn						
			420					425					430								
Thr	Val	Pro	Cys	Arg	Lys	Phe	Val	Lys	Ile	Asn	Asn	Ser	Thr	Asn	Glu						
		435				440						445									
Gly	Met	Asn	Val	Lys	Lys	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu						
	450					455					460										
Lys	Lys	Leu	Ser	Arg	Thr	Val	Lys	Phe	Thr	Tyr	Asp	Leu	Tyr	Leu	Val						
	465				470					475				480							
Thr	Asn	Gly	Lys	His	Gly	Lys	Lys	Val	Asn	Asn	Val	Trp	Asn	Gly	Met						
				485					490					495							
Ile	Gly	Glu	Val	Val	Tyr	Gln	Arg	Ala	Val	Met	Ala	Val	Gly	Ser	Leu						
			500					505					510								
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Val	Val	Asp	Phe	Ser	Val	Pro	Phe						
		515					520					525									

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Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val  
 530 535 540  
 Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met  
 545 550 555 560  
 Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu  
 565 570 575  
 Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys  
 580 585 590  
 Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu  
 595 600 605  
 Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly  
 610 615 620  
 Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile  
 625 630 635 640  
 Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu  
 645 650 655  
 Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg  
 660 665 670  
 Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly  
 675 680 685  
 Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr  
 690 695 700  
 Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu  
 705 710 715 720  
 Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn  
 725 730 735  
 Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser  
 740 745 750  
 Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly  
 755 760 765  
 Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln Phe Val Gly  
 770 775 780  
 Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys  
 785 790 795 800  
 His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn  
 805 810 815  
 Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu  
 820 825 830  
 Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys  
 835 840 845  
 Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser  
 850 855 860  
 Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys  
 865 870 875 880  
 Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys

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885					890					895					
Leu	Leu	Arg	Ser	Ala	Lys	Asn	Ile	Ser	Ser	Met	Ser	Asn	Met	Asn	Ser
			900					905					910		
Ser	Arg	Met	Asp	Ser	Pro	Lys	Arg	Ala	Ala	Asp	Phe	Ile	Gln	Arg	Gly
		915					920					925			
Ser	Leu	Ile	Met	Asp	Met	Val	Ser	Asp	Lys	Gly	Asn	Leu	Met	Tyr	Ser
	930					935					940				
Asp	Asn	Arg	Ser	Phe	Gln	Gly	Lys	Glu	Ser	Ile	Phe	Gly	Asp	Asn	Met
945						950					955				960
Asn	Glu	Leu	Gln	Thr	Phe	Val	Ala	Asn	Arg	Gln	Lys	Asp	Asn	Leu	Asn
				965					970						975
Asn	Tyr	Val	Phe	Gln	Gly	Gln	His	Pro	Leu	Thr	Leu	Asn	Glu	Ser	Asn
			980					985					990		
Pro	Asn	Thr	Val	Glu	Val	Ala	Val	Ser	Thr	Glu	Ser	Lys	Ala	Asn	Ser
		995					1000						1005		
Arg	Pro	Arg	Gln	Leu	Trp	Lys	Lys	Ser	Val	Asp	Ser	Ile	Arg	Gln	Asp
	1010					1015						1020			
Ser	Leu	Ser	Gln	Asn	Pro	Val	Ser	Gln	Arg	Asp	Glu	Ala	Thr	Ala	Glu
1025				1030							1035				1040
Asn	Arg	Thr	His	Ser	Leu	Lys	Ser	Pro	Arg	Tyr	Leu	Pro	Glu	Glu	Met
				1045					1050					1055	
Ala	His	Ser	Asp	Ile	Ser	Glu	Thr	Ser	Asn	Arg	Ala	Thr	Cys	His	Arg
			1060					1065						1070	
Glu	Pro	Asp	Asn	Ser	Lys	Asn	His	Lys	Thr	Lys	Asp	Asn	Phe	Lys	Arg
		1075					1080					1085			
Ser	Val	Ala	Ser	Lys	Tyr	Pro	Lys	Asp	Cys	Ser	Glu	Val	Glu	Arg	Thr
	1090					1095					1100				
Tyr	Leu	Lys	Thr	Lys	Ser	Ser	Pro	Arg	Asp	Lys	Ile	Tyr	Thr	Ile	
1105				1110					1115					1120	
Asp	Gly	Glu	Lys	Glu	Pro	Gly	Phe	His	Leu	Asp	Pro	Pro	Gln	Phe	Val
			1125						1130					1135	
Glu	Asn	Val	Thr	Leu	Pro	Glu	Asn	Val	Asp	Phe	Pro	Asp	Pro	Tyr	Gln
			1140					1145						1150	
Asp	Pro	Ser	Glu	Asn	Phe	Arg	Lys	Gly	Asp	Ser	Thr	Leu	Pro	Met	Asn
		1155					1160					1165			
Arg	Asn	Pro	Leu	His	Asn	Glu	Glu	Gly	Leu	Ser	Asn	Asn	Asp	Gln	Tyr
	1170					1175						1180			
Lys	Leu	Tyr	Ser	Lys	His	Phe	Thr	Leu	Lys	Asp	Lys	Gly	Ser	Pro	His
1185				1190							1195				1200
Ser	Glu	Thr	Ser	Glu	Arg	Tyr	Arg	Gln	Asn	Ser	Thr	His	Cys	Arg	Ser
				1205					1210					1215	
Cys	Leu	Ser	Asn	Met	Pro	Thr	Tyr	Ser	Gly	His	Phe	Thr	Met	Arg	Ser
			1220					1225					1230		
Pro	Phe	Lys	Cys	Asp	Ala	Cys	Leu	Arg	Met	Gly	Asn	Leu	Tyr	Asp	Ile
		1235					1240						1245		



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Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu  
 1250 1255 1260  
 Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln  
 1265 1270 1275 1280  
 Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val  
 1285 1290 1295  
 Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser  
 1300 1305 1310  
 Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu  
 1315 1320 1325  
 Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe  
 1330 1335 1340  
 Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp  
 1345 1350 1355 1360  
 His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg  
 1365 1370 1375  
 Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro  
 1380 1385 1390  
 Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr  
 1395 1400 1405  
 Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile  
 1410 1415 1420  
 Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser  
 1425 1430 1435 1440  
 Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu  
 1445 1450 1455  
 Met Pro Ser Ile Glu Ser Asp Val  
 1460

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 74 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCGGGCGCAG CGCCCCTTCC CCCTCGGACC  
 CTCCGGTGA CATG

60

74

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3155 base pairs
  - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAAGCCGGGC GTTCGGAGCT GTGCCC GGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTG GGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

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175										180										185										
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867														
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys															
			190					195					200																	
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915														
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val															
		205					210					215																		
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963														
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala															
	220					225					230																			
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC	1011														
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly															
235					240				245						250															
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059														
Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile															
				255					260					265																
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107														
Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser															
			270					275					280																	
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155														
Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys															
		285					290					295																		
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC	1203														
Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile															
	300					305					310																			
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251														
Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr															
315					320					325					330															
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299														
Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg															
				335					340					345																
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347														
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val															
			350					355					360																	
CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	1395														
Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys															
		365					370					375																		
ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443														
Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met															
		380				385					390																			
TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491														
Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr															
395					400					405					410															
GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539														
Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val															
				415					420					425																
AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	1587														
Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr															
			430				435						440																	

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TCG Ser	CCG Pro	GGC Gly 445	AGC Ser	CCC Pro	CGC Arg	CAC His	ACG Thr 450	GTG Val	CCT Pro	CAG Gln	TGT Cys	TGC Cys 455	TAC Tyr	GGC Gly	TTT Phe	1635
TGC Cys 460	ATC Ile	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys 465	CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met 470	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	1683
GAG Glu 475	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala 480	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly 485	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val 490	1731
AAC Asn	AAC Asn	AGC Ser	AAC Asn	AAG Lys 495	AAG Lys	GAG Glu	TGG Trp	AAT Asn	GGG Gly 500	ATG Met	ATG Met	GGC Gly	GAG Glu	CTG Leu 505	CTC Leu	1779
AGC Ser	GGG Gly	CAG Gln	GCA Ala 510	GAC Asp	ATG Met	ATC Ile	GTG Val 515	GCG Ala	CCG Pro	CTA Leu	ACC Thr	ATA Ile	AAC Asn	AAC Asn	GAG Glu	1827
CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile	GAG Glu	TTT Phe	TCC Ser 530	AAG Lys	CCC Pro	TTC Phe	AAG Lys	TAC Tyr 535	CAG Gln	GGC Gly	CTG Leu	1875
ACT Thr 540	ATT Ile	CTG Leu	GTC Val	AAG Lys	AAG Lys	GAG Glu 545	ATT Ile	CCC Pro	CGG Arg	AGC Ser	ACG Thr 550	CTG Leu	GAC Asp	TCG Ser	TTC Phe	1923
ATG Met 555	CAG Gln	CCG Pro	TTC Phe	CAG Gln	AGC Ser 560	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Leu 565	GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val 570	1971
CAC His	GTG Val	GTG Val	GCC Ala 575	GTG Val	ATG Met	CTG Leu	TAC Tyr	CTG Leu	CTG Leu 580	GAC Asp	CGC Arg	TTC Phe	AGC Ser	CCC Pro 585	TTC Phe	2019
GGC Gly	CGG Arg	TTC Phe	AAG Lys 590	GTG Val	AAC Asn	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala 600	CTG Leu	ACC Thr	2067
CTG Leu	TCC Ser	TCG Ser	GCC Ala 605	ATG Met	TGG Trp	TTC Phe	TCC Ser 610	TGG Trp	GGC Gly	GTC Val	CTG Leu	CTC Leu 615	AAC Asn	TCC Ser	GGC Gly	2115
ATC Ile 620	GGG Gly	GAA Glu	GGC Gly	GCC Ala	CCC Pro	AGA Arg 625	AGC Ser	TTC Phe	TCA Ser	GCG Ala	CGC Arg 630	ATC Ile	CTG Leu	GGC Gly	ATG Met	2163
GTG Val 635	TGG Trp	GCC Ala	GGC Gly	TTT Phe	GCC Ala 640	ATG Met	ATC Ile	ATC Ile	GTG Val	GCC Ala 645	TCC Ser	TAC Tyr	ACC Thr	GCC Ala	AAC Asn 650	2211
CTG Leu	GCG Ala	GCC Ala	TTC Phe	CTG Leu 655	GTG Val	CTG Leu	GAC Asp	CGG Arg	CCG Pro 660	GAG Glu	GAG Glu	CGC Arg	ATC Ile	ACG Thr 665	GGC Gly	2259
ATC Ile	AAC Asn	GAC Asp	CCT Pro 670	CGG Arg	CTG Leu	AGG Arg	AAC Asn 675	CCC Pro	TCG Ser	GAC Asp	AAG Lys	TTT Phe 680	ATC Ile	TAC Tyr	GCC Ala	2307
ACG Thr	GTG Val	AAG Lys 685	CAG Gln	AGC Ser	TCC Ser	GTG Val 690	GAT Asp	ATC Ile	TAC Tyr	TTC Phe	CGG Arg 695	CGC Arg	CAG Gln	GTG Val	GAG Glu	2355
CTG Leu 700	AGC Ser	ACC Thr	ATG Met	TAC Tyr	CGG Arg	CAT His 705	ATG Met	GAG Glu	AAG Lys	CAC His	AAC Asn 710	TAC Tyr	GAG Glu	AGT Ser	GCG Ala	2403

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GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCCC GGAGGCGCCC ACCTGCCCAG TTAGCCCGGC CAAGGACACT GATGGGTCTT	3087
GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCCAC CCTGGGCCTC	3147
CCGTCCGT	3155

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met 1	Ser	Thr	Met	Arg 5	Leu	Leu	Thr	Leu	Ala 10	Leu	Leu	Phe	Ser	Cys 15	Ser
Val	Ala	Arg	Ala 20	Ala	Cys	Asp	Pro	Lys 25	Ile	Val	Asn	Ile	Gly 30	Ala	Val
Leu	Ser	Thr 35	Arg	Lys	His	Glu	Gln 40	Met	Phe	Arg	Glu	Ala 45	Val	Asn	Gln
Ala	Asn 50	Lys	Arg	His	Gly	Ser 55	Trp	Lys	Ile	Gln	Leu 60	Asn	Ala	Thr	Ser
Val 65	Thr	His	Lys	Pro	Asn 70	Ala	Ile	Gln	Met	Ala 75	Leu	Ser	Val	Cys	Glu 80
Asp	Leu	Ile	Ser	Ser 85	Gln	Val	Tyr	Ala	Ile 90	Leu	Val	Ser	His	Pro 95	Pro
Thr	Pro	Asn 100	Asp	His	Phe	Thr	Pro	Thr 105	Pro	Val	Ser	Tyr	Thr 110	Ala	Gly
Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr	Thr	Arg	Met 125	Ser	Ile	Tyr
Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu	Arg	Thr 140	Val	Pro	Pro	Tyr
Ser 145	His	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met	Met 155	Arg	Val	Tyr	Ser	Trp 160
Asn	His	Ile	Ile 165	Leu	Leu	Val	Ser	Asp	Asp 170	His	Glu	Gly	Arg	Ala 175	Ala
Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu 185	Glu	Arg	Glu	Ser	Lys 190	Ala	Glu
Lys	Val	Leu 195	Gln	Phe	Asp	Pro	Gly 200	Thr	Lys	Asn	Val	Thr 205	Ala	Leu	Leu
Met	Glu 210	Ala	Lys	Glu	Leu	Glu 215	Ala	Arg	Val	Ile	Ile 220	Leu	Ser	Ala	Ser
Glu 225	Asp	Asp	Ala	Ala	Thr 230	Val	Tyr	Arg	Ala	Ala 235	Ala	Met	Leu	Asn	Met 240
Thr	Gly	Ser	Gly	Tyr 245	Val	Trp	Leu	Val	Gly 250	Glu	Arg	Glu	Ile	Ser 255	Gly
Asn	Ala	Leu	Arg 260	Tyr	Ala	Pro	Asp	Gly 265	Ile	Leu	Gly	Leu	Gln 270	Leu	Ile
Asn	Gly	Lys 275	Asn	Glu	Ser	Ala	His 280	Ile	Ser	Asp	Ala	Val 285	Gly	Val	Val
Ala	Gln 290	Ala	Val	His	Glu	Leu 295	Leu	Glu	Lys	Glu	Asn 300	Ile	Thr	Asp	Pro
Pro 305	Arg	Gly	Cys	Val	Gly 310	Asn	Thr	Asn	Ile	Trp 315	Lys	Thr	Gly	Pro	Leu 320
Phe	Lys	Arg	Val	Leu 325	Met	Ser	Ser	Lys	Tyr 330	Ala	Asp	Gly	Val	Thr 335	Gly
Arg	Val	Glu 340	Phe	Asn	Glu	Asp	Gly 345	Asp	Arg	Lys	Phe	Ala	Asn 350	Tyr	Ser

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Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn		
		355					360					365					
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly		
		370				375					380						
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile		
		385			390					395					400		
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser		
				405					410					415			
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys		
			420					425					430				
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg		
		435					440					445					
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile		
	450					455					460						
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala		
	465				470					475					480		
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys		
			485						490					495			
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met		
			500					505					510				
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu		
		515					520					525					
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys		
	530					535					540						
Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser		
	545				550					555					560		
Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met		
				565					570					575			
Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn		
			580					585					590				
Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp		
		595					600					605					
Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro		
	610					615					620						
Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala		
	625				630					635					640		
Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val		
				645					650					655			
Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu		
			660					665					670				
Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser		
		675					680					685					
Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg		
	690					695					700						

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His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala  
705 710 715 720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu  
725 730 735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu  
740 745 750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp  
755 760 765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe  
770 775 780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser  
785 790 795 800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val  
805 810 815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe  
820 825 830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met  
835 840 845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp  
850 855 860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe  
865 870 875 880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser  
885 890 895

Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn  
900 905 910

Leu Ser Asp Pro Ser Val Ser Thr Val Val  
915 920

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2540 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..2334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	48
Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	
1				5				10						15		
CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	96



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Arg	Ile	Pro	Val 20	Leu	Gly	Leu	Thr	Thr 25	Arg	Met	Ser	Ile	Tyr 30	Ser	Asp	
AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	144
Lys	Ser	Ile	His 35	Leu	Ser	Phe	Leu 40	Arg	Thr	Val	Pro	Pro 45	Tyr	Ser	His	
CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	192
Gln	Ser	Ser	Val	Trp	Phe	Glu 55	Met	Met	Arg	Val	Tyr 60	Ser	Trp	Asn	His	
ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	240
Ile	Ile	Leu	Leu	Val	Ser 70	Asp	Asp	His	Glu	Gly 75	Arg	Ala	Ala	Gln	Lys 80	
CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	288
Arg	Leu	Glu	Thr 85	Leu	Leu	Glu	Glu	Arg	Glu 90	Ser	Lys	Ser	Lys	Lys 95	Arg	
AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	336
Asn	Tyr	Glu	Asn 100	Leu	Asp	Gln	Leu	Ser 105	Tyr	Asp	Asn	Lys	Arg 110	Gly	Pro	
AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	384
Lys	Ala	Glu	Lys 115	Val	Leu	Gln	Phe 120	Asp	Pro	Gly	Thr	Lys 125	Asn	Val	Thr	
GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	432
Ala	Leu	Leu	Met	Glu	Ala	Lys 135	Glu	Leu	Glu	Ala	Arg 140	Val	Ile	Ile	Leu	
TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	480
Ser	Ala	Ser	Glu	Asp	Asp 150	Ala	Ala	Thr	Val	Tyr 155	Arg	Ala	Ala	Ala	Met 160	
CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	528
Leu	Asn	Met	Thr 165	Gly	Asn	Thr	Asn	Ile	Trp 170	Lys	Thr	Gly	Pro	Leu 175	Phe	
AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	576
Lys	Arg	Val	Leu 180	Met	Ser	Ser	Lys	Tyr 185	Ala	Asp	Gly	Val	Thr 190	Gly	Arg	
GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	624
Val	Glu	Phe	Asn 195	Glu	Asp	Gly	Asp 200	Arg	Lys	Phe	Ala	Asn 205	Tyr	Ser	Ile	
ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	672
Met	Asn	Leu	Gln	Asn	Arg	Lys 215	Leu	Val	Gln	Val	Gly 220	Ile	Tyr	Asn	Gly	
ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	720
Thr	His	Val	Ile	Pro	Asn 230	Asp	Arg	Lys	Ile	Ile	Trp 235	Pro	Gly	Gly	Glu 240	
ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	768
Thr	Glu	Lys	Pro	Arg 245	Gly	Tyr	Gln	Met	Ser 250	Thr	Arg	Leu	Lys 255	Ile	Val	
ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	816
Thr	Ile	His	Gln 260	Glu	Pro	Phe	Val	Tyr 265	Val	Lys	Pro	Thr	Leu 270	Ser	Asp	
GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	864
Gly	Thr	Cys 275	Lys	Glu	Glu	Phe	Thr 280	Val	Asn	Gly	Asp	Pro 285	Val	Lys	Lys	

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GTG Val 290	ATC Ile	TGC Cys	ACC Thr	GGG Gly	CCC Pro	AAC Asn 295	GAC Asp	ACG Thr	TCG Ser	CCG Pro	GGC Gly 300	AGC Ser	CCC Pro	CGC Arg	CAC His	912
ACG Thr 305	GTG Val	CCT Pro	CAG Gln	TGT Cys	TGC Cys 310	TAC Tyr	GGC Gly	TTT Phe	TGC Cys	ATC Ile 315	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys 320	960
CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met 325	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	GAG Glu 330	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala 335	GAT Asp	1008
GGC Gly	AAG Lys	TTC Phe	GGC Gly 340	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val 345	AAC Asn	AAC Asn	AGC Ser	AAC Asn	AAG Lys 350	AAG Lys	GAG Glu	1056
TGG Trp	AAT Asn 355	GGG Gly	ATG Met	ATG Met	GGC Gly	GAG Glu	CTG Leu 360	CTC Leu	AGC Ser	GGG Gly	CAG Gln 365	GCA Ala	GAC Asp	ATG Met	ATC Ile	1104
GTG Val 370	GCG Ala	CCG Pro	CTA Leu	ACC Thr	ATA Ile	AAC Asn 375	AAC Asn	GAG Glu	CGC Arg	GCG Ala	CAG Gln 380	TAC Tyr	ATC Ile	GAG Glu	TTT Phe	1152
TCC Ser 385	AAG Lys	CCC Pro	TTC Phe	AAG Lys	TAC Tyr 390	CAG Gln	GGC Gly	CTG Leu	ACT Thr	ATT Ile 395	CTG Leu	GTC Val	AAG Lys	AAG Lys	GAG Glu 400	1200
ATT Ile	CCC Pro	CGG Arg	AGC Ser	ACG Thr 405	CTG Leu	GAC Asp	TCG Ser	TTC Phe	ATG Met 410	CAG Gln	CCG Pro	TTC Phe	CAG Gln	AGC Ser 415	ACA Thr	1248
CTG Leu	TGG Trp	CTG Leu	CTG Leu 420	GTG Val	GGG Gly	CTG Leu	TCG Ser 425	GTG Val	CAC His	GTG Val	GTG Val	GCC Ala	GTG Val 430	ATG Met	CTG Leu	1296
TAC Tyr	CTG Leu	CTG Leu 435	GAC Asp	CGC Arg	TTC Phe	AGC Ser	CCC Pro 440	TTC Phe	GGC Gly	CGG Arg	TTC Phe	AAG Lys 445	GTG Val	AAC Asn	AGC Ser	1344
GAG Glu 450	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp 455	GCA Ala	CTG Leu	ACC Thr	CTG Leu	TCC Ser	TCG Ser 460	GCC Ala	ATG Met	TGG Trp	TTC Phe	1392
TCC Ser 465	TGG Trp	GGC Gly	GTC Val	CTG Leu	CTC Leu 470	AAC Asn	TCC Ser	GGC Gly	ATC Ile	GGG Gly 475	GAA Glu	GGC Gly	GCC Ala	CCC Pro	AGA Arg 480	1440
AGC Ser	TTC Phe	TCA Ser	GCG Ala	CGC Arg 485	ATC Ile	CTG Leu	GGC Gly	ATG Met	GTG Val 490	TGG Trp	GCC Ala	GGC Gly	TTT Phe	GCC Ala 495	ATG Met	1488
ATC Ile	ATC Ile	GTG Val	GCC Ala	TCC Ser	TAC Tyr	ACC Thr	GCC Ala 505	AAC Asn	CTG Leu	GCG Ala	GCC Ala	TTC Phe	CTG Leu 510	GTG Val	CTG Leu	1536
GAC Asp	CGG Arg	CCG Pro	GAG Glu 515	GAG Glu	CGC Arg	ATC Ile	ACG Thr 520	GGC Gly	ATC Ile	AAC Asn	GAC Asp	CCT Pro 525	CGG Arg	CTG Leu	AGG Arg	1584
AAC Asn 530	CCC Pro	TCG Ser	GAC Asp	AAG Lys	TTT Phe	ATC Ile 535	TAC Tyr	GCC Ala	ACG Thr	GTG Val	AAG Lys 540	CAG Gln	AGC Ser	TCC Ser	GTG Val	1632
GAT Asp 545	ATC Ile	TAC Tyr	TTC Phe	CGG Arg	CGC Arg 550	CAG Gln	GTG Val	GAG Glu	CTG Leu	AGC Ser 555	ACC Thr	ATG Met	TAC Tyr	CGG Arg	CAT His 560	1680

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ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val 565 570 575	1728
AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu 580 585 590	1776
TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe 595 600 605	1824
TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys 610 615 620	1872
CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met 625 630 635 640	1920
GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg 645 650 655	1968
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe 660 665 670	2016
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile 675 680 685	2064
GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln 690 695 700	2112
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg 705 710 715 720	2160
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg 725 730 735	2208
GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC Ala Ile Thr Ser Thr Leu Ala Ser Phe Lys Arg Arg Arg Ser Ser 740 745 750	2256
AAA GAC ACG CAG TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu 755 760 765	2304
TCA GAT CCC TCG GTC AGC ACC GTG GTG TGAGGCCCCC GGAGGCGCCC Ser Asp Pro Ser Val Ser Thr Val Val 770 775	2351
ACCTGCCCAG TTAGCCCGGC CAAGGACACT GATGGGTCCT GCTGCTCGGG AAGGCCTGAG	2411
GGAAGCCCAC CCGCCCCAGA GACTGCCCAC CCTGGGCCTC CCGTCCGTCC GCCCGCCCAC	2471
CCCGCTGCCT GGCGGGCAGC CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG	2531
GGGCAGAGC	2540

(2) INFORMATION FOR SEQ ID NO:16:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	1	5	10	15
Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	20	25	30	
Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	35	40	45	
Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	Asn	His	50	55	60	
Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	65	70	75	80
Arg	Leu	Glu	Thr	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	85	90	95		
Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	100	105	110	
Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	115	120	125	
Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	130	135	140	
Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	145	150	155	160
Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	165	170	175	
Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	180	185	190	
Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	195	200	205	
Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	210	215	220	
Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	225	230	235	240
Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	245	250	255	
Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	260	265	270	
Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	275	280	285	
Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	290	295	300	
Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys				

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305		310		315		320
Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp						
	325			330		335
Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu						
	340		345			350
Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile						
	355		360			365
Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe						
	370		375			380
Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu						
	385		390			395
Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr						
	405			410		415
Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu						
	420		425			430
Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser						
	435		440			445
Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe						
	450		455			460
Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg						
	465		470			475
Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met						
	485			490		495
Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu						
	500		505			510
Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg						
	515		520			525
Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val						
	530		535			540
Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His						
	545		550			555
Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val						
	565		570			575
Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu						
	580		585			590
Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe						
	595		600			605
Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys						
	610		615			620
Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met						
	625		630			635
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg						
	645		650			655
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe						

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660	665	670
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile		
675	680	685
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln		
690	695	700
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg		
705	710	715
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg		
725	730	735
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser		
740	745	750
Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu		
755	760	765
Ser Asp Pro Ser Val Ser Thr Val Val		
770	775	

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 595 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..576

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC	48
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1 5 10 15	
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC	96
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20 25 30	
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC	144
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35 40 45	
GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG	192
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50 55 60	
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA	240
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65 70 75 80	
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG	288
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
85 90 95	

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GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC	336
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG	384
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT	432
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG	480
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	
CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT	528
Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly	
165 170 175	
GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA	583
Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	
180 185 190	
AGGAATGTCA CG	595

## (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1 5 10 15	
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20 25 30	
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35 40 45	
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50 55 60	
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65 70 75 80	
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
85 90 95	
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	

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Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly  
                   165                                  170                                  175

Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp  
                   180                                  185                                  190

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3935 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3030

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1                                  5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15                                  20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30                                  35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45                                  50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60                                  65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75                                  80	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	100
95                                  100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	115
110                                  115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	



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125	130	135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150			723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170			771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185			819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190 195 200			867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215			915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230			963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235 240 245 250			1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255 260 265			1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270 275 280			1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285 290 295			1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300 305 310			1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315 320 325 330			1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335 340 345			1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350 355 360			1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365 370 375			1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380 385 390			1443

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TCC Ser 395	ACC Thr	AGA Arg	CTG Leu	AAG Lys	ATT Ile	GTG Val	ACG Thr	ATC Ile	CAC His	CAG Gln	GAG Glu	CCC Pro	TTC Phe	GTG Val	TAC Tyr	1491
					400					405					410	
GTC Val	AAG Lys	CCC Pro	ACG Thr	CTG Leu	AGT Ser	GAT Asp	GGG Gly	ACA Thr	TGC Cys	AAG Lys	GAG Glu	GAG Glu	TTC Phe	ACA Thr	GTC Val	1539
				415					420					425		
AAC Asn	GGC Gly	GAC Asp	CCA Pro	GTC Val	AAG Lys	AAG Lys	GTG Val	ATC Ile	TGC Cys	ACC Thr	GGG Gly	CCC Pro	AAC Asn	GAC Asp	ACG Thr	1587
			430					435					440			
TCG Ser	CCG Pro	GGC Gly	AGC Ser	CCC Pro	CGC Arg	CAC His	ACG Thr	GTG Val	CCT Pro	CAG Gln	TGT Cys	TGC Cys	TAC Tyr	GGC Gly	TTT Phe	1635
		445					450					455				
TGC Cys	ATC Ile	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys	CTG Leu	GCA Ala	CGG Arg	ACC Thr	ATG Met	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	1683
	460					465					470					
GAG Glu	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly	ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val	1731
	475				480					485					490	
AAC Asn	AAC Asn	AGC Ser	AAC Asn	AAG Lys	AAG Lys	GAG Glu	TGG Trp	AAT Asn	GGG Gly	ATG Met	ATG Met	GGC Gly	GAG Glu	CTG Leu	CTC Leu	1779
				495					500					505		
AGC Ser	GGG Gly	CAG Gln	GCA Ala	GAC Asp	ATG Met	ATC Ile	GTG Val	GCG Ala	CCG Pro	CTA Leu	ACC Thr	ATA Ile	AAC Asn	AAC Asn	GAG Glu	1827
			510					515					520			
CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro	TTC Phe	AAG Lys	TAC Tyr	CAG Gln	GGC Gly	CTG Leu	1875
		525					530					535				
ACT Thr	ATT Ile	CTG Leu	GTC Val	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp	TCG Ser	TTC Phe	1923
	540					545					550					
ATG Met	CAG Gln	CCG Pro	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Val	GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val	1971
	555				560					565					570	
CAC His	GTG Val	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg	TTC Phe	AGC Ser	CCC Pro	TTC Phe	2019
				575					580					585		
GGC Gly	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala	CTG Leu	ACC Thr		2067
			590					595				600				
CTG Leu	TCC Ser	TCG Ala	GCC Met	ATG Trp	TGG Phe	TTC Ser	TCC Trp	TGG Gly	GGC Val	GTC Leu	CTG Leu	CTC Leu	AAC Asn	TCC Ser	GGC Gly	2115
		605				610						615				
ATC Ile	GGG Glu	GAA Glu	GGC Gly	GCC Ala	CCC Pro	AGA Arg	AGC Ser	TTC Phe	TCA Ser	GCG Ala	CGC Arg	ATC Ile	CTG Leu	GGC Gly	ATG Met	2163
	620					625					630					
GTG Val	TGG Trp	GCC Ala	GGC Gly	TTT Phe	GCC Ala	ATG Met	ATC Ile	ATC Ile	GTG Val	GCC Ala	TCC Ser	TAC Tyr	ACC Thr	GCC Ala	AAC Asn	2211
	635				640					645					650	
CTG Leu	GCG Ala	GCC Ala	TTC Phe	CTG Leu	GTG Val	CTG Leu	GAC Asp	CGG Arg	CCG Pro	GAG Glu	GAG Glu	CGC Arg	ATC Ile	ACG Thr	GGC Gly	2259
				655					660					665		

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ATC Ile	AAC Asn	GAC Asp	CCT Pro 670	CGG Arg	CTG Leu	AGG Arg	AAC Asn	CCC Pro 675	TCG Ser	GAC Asp	AAG Lys	TTT Phe	ATC Ile 680	TAC Tyr	GCC Ala	2307	
ACG Thr	GTG Val	AAG Lys 685	CAG Gln	AGC Ser	TCC Ser	GTG Val	GAT Asp 690	ATC Ile	TAC Tyr	TTC Phe	CGG Arg 695	CGC Arg	CAG Gln	GTG Val	GAG Glu	2355	
CTG Leu	AGC Ser 700	ACC Thr	ATG Met	TAC Tyr	CGG Arg	CAT His 705	ATG Met	GAG Glu	AAG Lys	CAC His	AAC Asn 710	TAC Tyr	GAG Glu	AGT Ser	GCG Ala	2403	
GCG Ala 715	GAG Glu	GCC Ala	ATC Ile	CAG Gln	GCC Ala 720	GTG Val	AGA Arg	GAC Asp	AAC Asn	AAG Lys 725	CTG Leu	CAT His	GCC Ala	TTC Phe	ATC Ile 730	2451	
TGG Trp	GAC Asp	TCG Ser	GCG Ala	GTG Val 735	CTG Leu	GAG Glu	TTC Phe	GAG Glu 740	GCC Ala	TCG Ser	CAG Gln	AAG Lys	TGC Cys	GAC Asp 745	CTG Leu	2499	
GTG Val	ACG Thr	ACT Thr	GGA Gly 750	GAG Glu	CTG Leu	TTT Phe	TTC Phe	CGC Arg 755	TCG Ser	GGC Gly	TTC Phe	GGC Gly	ATA Ile 760	GGC Gly	ATG Met	2547	
CGC Arg	AAA Lys	GAC Asp 765	AGC Ser	CCC Pro	TGG Trp	AAG Lys	CAG Gln 770	AAC Asn	GTC Val	TCC Ser	CTG Leu	TCC Ser 775	ATC Ile	CTC Leu	AAG Lys	2595	
TCC Ser	CAC His 780	GAG Glu	AAT Asn	GGC Gly	TTC Phe	ATG Met 785	GAA Glu	GAC Asp	CTG Leu	GAC Asp	AAG Lys 790	ACG Thr	TGG Trp	GTT Val	CGG Arg	2643	
TAT Tyr 795	CAG Gln	GAA Glu	TGT Cys	GAC Asp	TCG Ser 800	CGC Arg	AGC Ser	AAC Asn	GCC Ala	CCT Pro 805	GCG Ala	ACC Thr	CTT Leu	ACT Thr	TTT Phe 810	2691	
GAG Glu	AAC Asn	ATG Met	GCC Ala 815	GGG Gly	GTC Val	TTC Phe	ATG Met	CTG Leu 820	GTA Val	GCT Ala	GGG Gly	GGC Gly	ATC Ile 825	GTG Val	GCC Ala	2739	
GGG Gly	ATC Ile	TTC Phe	CTG Leu 830	ATT Ile	TTC Phe	ATC Ile	GAG Glu 835	ATT Ile	GCC Ala	TAC Tyr	AAG Lys	CGG Arg 840	CAC His	AAG Lys	GAT Asp	2787	
GCT Ala	CGC Arg	CGG Arg 845	AAG Lys	CAG Gln	ATG Met	CAG Gln	CTG Leu 850	GCC Ala	TTT Phe	GCC Ala	GCC Ala 855	GTT Val	AAC Asn	GTG Val	TGG Trp	2835	
CGG Arg 860	AAG Lys	AAC Asn	CTG Leu	CAG Gln	GAT Asp	AGA Arg 865	AAG Lys	AGT Ser	GGT Gly	AGA Arg	GCA Ala 870	GAG Glu	CCT Pro	GAC Asp	CCT Pro	2883	
AAA Lys 875	AAG Lys	AAA Lys	GCC Ala	ACA Thr	TTT Phe 880	AGG Arg	GCT Ala	ATC Ile	ACC Thr	TCC Ser 885	ACC Thr	CTG Leu	GCT Ala	TCC Ser	AGC Ser 890	2931	
TTC Phe	AAG Lys	AGG Arg	CGT Arg 895	AGG Arg	TCC Ser	TCC Ser	AAA Lys	GAC Asp	ACG Thr 900	CAG Gln	TAC Tyr	CAT His	CCC Pro	ACT Thr 905	GAT Asp	2979	
ATC Ile	ACG Thr	GGC Gly 910	CCG Pro	CTC Leu	AAC Asn	CTC Leu	TCA Ser	GAT Asp 915	CCC Pro	TCG Ser	GTC Val	AGC Ser	ACC Thr 920	GTG Val	GTG Val	3027	
TGAGGCCCCC			GGAGGCGCCC			ACCTGCCCAG			TTAGCCCGGC			CAAGGACACT			GATGGGTCCT		3087
GCTGCTCGGG			AAGGCCTGAG			GGAAGCCCAC			CCGCCCCAGA			GACTGCCCAC			CCTGGGCCTC		3147

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CCGTCCGTCC  GCCCGCCAC  CCCGCTGCCT  GCGGGGCAGC  CCCTGCTGGA  CCAAGGTGCG      3207
GACCGGAGCG  GCTGAGGACG  GGGCAGAGCT  GAGTCGGCTG  GGCAGGGCCG  CAGGGCGCTC      3267
CGGCAGAGGC  AGGCCCCCTG  GGTCTCTGAG  CAGTGGGGAG  CGGGGGCTAA  CTGCCCCCAG      3327
GCGGAGGGGC  TTGGAGCAGA  GACGGCAGCC  CCATCCTTCC  CGCAGCACCA  GCCTGAGCCA      3387
CAGTGGGGCC  CATGGCCCCA  GCTGGCTGGG  TCGCCCCTCC  TCGGGCGCCT  GCGCTCCTCT      3447
GCAGCCTGAG  CTCCACCCTC  CCCTCTTCTT  GCGGCACCGC  CCACCAAACA  CCCCCTCTGC      3507
CCCTTGACGC  CACACGCCGG  GGCTGGCGCT  GCCCTCCCCC  ACGGCCGTCC  CTGACTTCCC      3567
AGCTGGCAGC  GCCTCCCGCC  GCCTCGGGCC  GCCTCCTCCA  GAATCGAGAG  GGCTGAGCCC      3627
CTCCTCTCCT  CGTCCGGCCT  GCAGCACAGA  AGGGGGCCTC  CCCGGGGGTC  CCCGGACGCT      3687
GGCTCGGGAC  TGTCTTCAAC  CCTGCCCTGC  ACCTTGGGCA  CGGGAGAGCG  CCACCCGCCC      3747
GCCCCCGCCC  TCGCTCCGGG  TCGTGACCG  GCCCGCCACC  TTGTACAGAA  CCAGCACTCC      3807
CAGGGCCCCG  GCGCGTGCTT  TCCCCGTGCG  CAGCCGCGCT  CTGCCCCTCC  GTCCCCAGGG      3867
TGCAGGCGCG  CACCGCCCAA  CCCCCACCTC  CCGGTGTATG  CAGTGGTGAT  GCCTAAAGGA      3927
ATGTCACG                                     3935

```

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 922 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1             5             10             15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
          20             25             30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
      35             40             45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
      50             55             60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
      65             70             75             80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
          85             90             95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
          100             105             110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
          115             120             125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
          130             135             140

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Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
 145 150 155 160  
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
 165 170 175  
 Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
 180 185 190  
 Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
 195 200 205  
 Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
 210 215 220  
 Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
 225 230 235 240  
 Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly  
 245 250 255  
 Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
 260 265 270  
 Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
 275 280 285  
 Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
 290 295 300  
 Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
 305 310 315 320  
 Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
 325 330 335  
 Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
 340 345 350  
 Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
 355 360 365  
 Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
 370 375 380  
 Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
 385 390 395 400  
 Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
 405 410 415  
 Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
 420 425 430  
 Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
 435 440 445  
 His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
 450 455 460  
 Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
 465 470 475 480  
 Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
 485 490 495  
 Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met

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500					505					510					
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu
		515					520					525			
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys
		530				535					540				
Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser
545					550					555					560
Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met
				565					570					575	
Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn
			580					585					590		
Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp
		595					600					605			
Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro
		610				615					620				
Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala
625						630					635				640
Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val
				645					650					655	
Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu
			660					665					670		
Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser
		675					680					685			
Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg
		690				695					700				
His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala
705						710					715				720
Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu
				725					730					735	
Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu
			740					745					750		
Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp
		755					760					765			
Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe
		770				775					780				
Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser
785						790					795				800
Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val
				805					810					815	
Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe
			820					825					830		
Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met
		835					840					845			
Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp

CAAGCCGGGGC	GTTCGGAGCT	GTGCCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCC		60										
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC		120										
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGCCG	GGCGAGCGCA		180										
GGACGGCCCCG	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG		240										
CCAGGCCCCGC	GGCCCGAGCC	C	ATG	AGC	ACC	ATG	CGC	CTG	CTG	ACG	CTC	GCC		291			
			Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala		10			
			1				5										
CTG	CTG	TTC	TCC	TGC	TCC	GTC	GCC	CGT	GCC	GCG	TGC	GAC	CCC	AAG	ATC		339
Leu	Leu	Phe	Ser	Cys	Ser	Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile		25
				15					20								
GTC	AAC	ATT	GGC	GCG	GTG	CTG	AGC	ACG	CGG	AAG	CAC	GAG	CAG	ATG	TTC		387
Val	Asn	Ile	Gly	Ala	Val	Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe		40
			30					35					40				
CGC	GAG	GCC	GTG	AAC	CAG	GCC	AAC	AAG	CGG	CAC	GGC	TCC	TGG	AAG	ATT		435
Arg	Glu	Ala	Val	Asn	Gln	Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile		55
		45					50					55					
CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG		483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met		70
	60					65					70						
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC		531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile		90
	75				80					85					90		
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT		579

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Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTG	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	
			190					195					200			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
	205						210					215				
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
	220					225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	GTG	TGG	CTG	GTC	GGC	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	
235					240				245						250	
GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	GCC	CCA	GAC	GGC	ATC	1059
Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	
				255				260						265		
CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	TCG	GCC	CAC	ATC	AGC	1107
Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	
			270					275					280			
GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	GAG	CTC	CTC	GAG	AAG	1155
Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	
		285					290					295				
GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	GGC	AAC	ACC	AAC	ATC	1203
Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	
	300					305					310					
TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	1251
Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	
315					320					325					330	
GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	1299
Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	
				335				340						345		
AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	1347
Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	



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350						355						360						
CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	1395		
Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys			
		365					370					375						
ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	1443		
Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met			
		380				385					390							
TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	1491		
Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr			
					400					405					410			
GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	1539		
Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val			
				415					420					425				
AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	1587		
Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr			
			430					435					440					
TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	1635		
Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe			
		445					450					455						
TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	1683		
Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr			
		460				465					470							
GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731		
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val			
					480					485					490			
AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779		
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu			
				495					500					505				
AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827		
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu			
			510					515					520					
CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875		
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu			
		525					530					535						
ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923		
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe			
		540				545					550							
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971		
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val			
					560					565					570			
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019		
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe			
				575					580					585				
GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067		
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr			
			590					595					600					
CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115		
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly			
		605					610					615						
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163		

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Ile 620	Gly	Glu	Gly	Ala	Pro	Arg 625	Ser	Phe	Ser	Ala	Arg 630	Ile	Leu	Gly	Met	
GTG 635	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala 640	Met	Ile	Ile	Val	Ala 645	Ser	Tyr	Thr	Ala	Asn 650	
CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259
Leu	Ala	Ala	Phe	Leu 655	Val	Leu	Asp	Arg	Pro 660	Glu	Glu	Arg	Ile	Thr	Gly 665	
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro 670	Arg	Leu	Arg	Asn	Pro 675	Ser	Asp	Lys	Phe	Ile	Tyr	Ala 680	
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys 685	Gln	Ser	Ser	Val	Asp 690	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His 705	Met	Glu	Lys	His	Asn 710	Tyr	Glu	Ser	Ala	
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
Ala	Glu	Ala	Ile	Gln	Ala 720	Val	Arg	Asp	Asn	Lys 725	Leu	His	Ala	Phe	Ile 730	
TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
Trp	Asp	Ser	Ala	Val 735	Leu	Glu	Phe	Glu	Ala 740	Ser	Gln	Lys	Cys	Asp	Leu 745	
GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	ATG	2547
Val	Thr	Thr	Gly 750	Glu	Leu	Phe	Phe	Arg 755	Ser	Gly	Phe	Gly	Ile	Gly	Met 760	
CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG	2595
Arg	Lys	Asp 765	Ser	Pro	Trp	Lys	Gln	Asn 770	Val	Ser	Leu	Ser	Ile	Leu	Lys	
TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG	2643
Ser	His	Glu	Asn	Gly	Phe	Met 785	Glu	Asp	Leu	Asp	Lys 790	Thr	Trp	Val	Arg	
TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT	2691
Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala 805	Pro	Ala	Thr	Leu	Thr	Phe 810	
GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	2739
Glu	Asn	Met	Ala	Gly 815	Val	Phe	Met	Leu	Val 820	Ala	Gly	Gly	Ile	Val	Ala 825	
GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	2787
Gly	Ile	Phe	Leu 830	Ile	Phe	Ile	Glu	Ile 835	Ala	Tyr	Lys	Arg	His	Lys	Asp 840	
GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	2835
Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala 850	Phe	Ala	Ala	Val	Asn	Val	Trp 855	
CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	2883
Arg	Lys	Asn	Leu	Gln	Asp	Arg 865	Lys	Ser	Gly	Arg	Ala 870	Glu	Pro	Asp	Pro	
AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	2931
Lys	Lys	Lys	Ala	Thr	Phe 880	Arg	Ala	Ile	Thr	Ser 885	Thr	Leu	Ala	Ser	Ser 890	

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TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT	2979
Phe Lys Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu	
895 900 905	
CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC	3027
Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro	
910 915 920	
CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC	3075
Pro Pro Ser Leu Arg Val Arg Arg Pro Ala Thr Leu Tyr Arg Thr	
925 930 935	
AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT	3123
Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala	
940 945 950	
CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC	3171
Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr	
955 960 965 970	
TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG	3211
Ser Arg Cys Met Gln Trp	
975	

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 976 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	

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165					170					175					
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu
			180					185					190		
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu
		195					200					205			
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser
	210					215					220				
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met
225					230				235						240
Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly
			245						250					255	
Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile
			260					265					270		
Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val
		275					280					285			
Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro
	290					295					300				
Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu
305					310					315					320
Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly
			325						330					335	
Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser
			340				345						350		
Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn
	355					360						365			
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly
	370					375						380			
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile
385					390					395					400
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser
			405					410						415	
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys
			420				425						430		
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg
		435					440					445			
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile
	450					455					460				
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala
465					470					475					480
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys
			485					490					495		
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met
			500					505					510		
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu

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515				520				525							
Phe 530	Ser	Lys	Pro	Phe	Lys	Tyr 535	Gln	Gly	Leu	Thr	Ile 540	Leu	Val	Lys	Lys
Glu 545	Ile	Pro	Arg	Ser	Thr 550	Leu	Asp	Ser	Phe	Met 555	Gln	Pro	Phe	Gln	Ser 560
Thr	Leu	Trp	Leu	Leu 565	Val	Gly	Leu	Ser	Val 570	His	Val	Val	Ala	Val 575	Met
Leu	Tyr	Leu	Leu 580	Asp	Arg	Phe	Ser	Pro 585	Phe	Gly	Arg	Phe	Lys 590	Val	Asn
Ser	Glu	Glu 595	Glu	Glu	Glu	Asp	Ala 600	Leu	Thr	Leu	Ser	Ser 605	Ala	Met	Trp
Phe 610	Ser	Trp	Gly	Val	Leu	Leu 615	Asn	Ser	Gly	Ile	Gly 620	Glu	Gly	Ala	Pro
Arg 625	Ser	Phe	Ser	Ala	Arg 630	Ile	Leu	Gly	Met	Val 635	Trp	Ala	Gly	Phe	Ala 640
Met	Ile	Ile	Val	Ala 645	Ser	Tyr	Thr	Ala	Asn 650	Leu	Ala	Ala	Phe	Leu 655	Val
Leu	Asp	Arg	Pro 660	Glu	Glu	Arg	Ile	Thr 665	Gly	Ile	Asn	Asp	Pro 670	Arg	Leu
Arg	Asn 675	Pro	Ser	Asp	Lys	Phe	Ile 680	Tyr	Ala	Thr	Val	Lys 685	Gln	Ser	Ser
Val 690	Asp	Ile	Tyr	Phe	Arg	Arg 695	Gln	Val	Glu	Leu	Ser 700	Thr	Met	Tyr	Arg
His 705	Met	Glu	Lys	His	Asn 710	Tyr	Glu	Ser	Ala	Ala 715	Glu	Ala	Ile	Gln	Ala 720
Val	Arg	Asp	Asn 725	Lys	Leu	His	Ala	Phe	Ile 730	Trp	Asp	Ser	Ala	Val 735	Leu
Glu	Phe	Glu	Ala 740	Ser	Gln	Lys	Cys	Asp 745	Leu	Val	Thr	Thr	Gly 750	Glu	Leu
Phe 755	Phe	Arg	Ser	Gly	Phe	Gly	Ile 760	Gly	Met	Arg	Lys	Asp 765	Ser	Pro	Trp
Lys 770	Gln	Asn	Val	Ser	Leu	Ser 775	Ile	Leu	Lys	Ser	His 780	Glu	Asn	Gly	Phe
Met 785	Glu	Asp	Leu	Asp	Lys 790	Thr	Trp	Val	Arg	Tyr 795	Gln	Glu	Cys	Asp	Ser 800
Arg	Ser	Asn	Ala 805	Pro	Ala	Thr	Leu	Thr	Phe 810	Glu	Asn	Met	Ala	Gly 815	Val
Phe	Met	Leu	Val 820	Ala	Gly	Gly	Ile	Val 825	Ala	Gly	Ile	Phe	Leu	Ile	Phe 830
Ile	Glu	Ile 835	Ala	Tyr	Lys	Arg	His 840	Lys	Asp	Ala	Arg	Arg 845	Lys	Gln	Met
Gln 850	Leu	Ala	Phe	Ala	Ala	Val	Asn 855	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp 860
Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe

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865	870	875	880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser	885	890	895
Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro	900	905	910
Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val	915	920	925
Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg	930	935	940
Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln	945	950	955
Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	965	970	975

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4361 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3141

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGCCGGGC GTTCGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGAGCC CGCGGGGCCG GCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	

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CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
60						65				70						
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
75				80					85						90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
			95						100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
140						145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
		220				225					230					
CTG	GAG	GCC	CGG	GTC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC		1011
Leu	Glu	Ala	Arg	Val	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala		
235				240					245					250		
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
				255					260					265		
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
			270					275					280			
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
		285				290						295				
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
		300				305					310					
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
315					320					325					330	

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GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu 335 340 345	1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn 350 355 360	1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln 365 370 375	1395
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390	1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410	1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425	1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440	1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr 445 450 455	1635
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln 460 465 470	1683
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr 475 480 485 490	1731
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly 495 500 505	1779
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met 510 515 520	1827
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu 525 530 535	1875
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe 540 545 550	1923
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser 555 560 565 570	1971
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu 575 580 585	2019
GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp 590 595 600	2067



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CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	
		605					610					615				
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	
	620					625					630					
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
635					640					645					650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660					665		
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
			670					675					680			
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
		685					690					695				
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
	700					705					710					
CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	2451
Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	
715					720					725					730	
AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	2499
Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	
				735					740					745		
CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	2547
Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	
			750					755					760			
CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	2595
Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	
		765					770					775				
TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	2643
Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	
	780					785					790					
CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	2691
Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	
795					800					805					810	
AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	2739
Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	
				815					820					825		
GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	2787
Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	
			830					835					840			
GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	2835
Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	
		845					850					855				
AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	2883
Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	
	860					865					870					

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GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser 910 915 920	3027
ACC GGG GGT GGA CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu 925 930 935	3075
CCG CGA CGC GCT ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser 940 945 950	3123
CGT CAT AGG GAG AGC TGAGACTCCC CGCCCGCCCT CCTCTGCCCC CTCCCCGCA Arg His Arg Glu Ser 955 960	3178
GACAGACAGA CAGACGGACG GGACAGCGGC CCGGCCACAG CAGAGCCCCG GAGCACCACG	3238
GGGTCTGGGG AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG	3298
CCGGCTGGCC GGTCCACCCC GTCCCGGCCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG	3358
CGCCTTGTCT GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCG	3418
TCAACCTCTC AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG	3478
CCCAGTTAGC CCGGCCAAGG AACTGATGG GTCCTGCTGC TCGGAAGGC CTGAGGGAAG	3538
CCCACCCGCC CCAGAGACTG CCCACCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC	3598
TGCCTGGCGG GCAGCCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA	3658
GAGCTGAGTC GGCTGGGCAG GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT	3718
CTGAGCAGTG GGGAGCGGGG GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG	3778
CAGCCCCATC CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCAGCTGG	3838
CTGGGTCGCC CTTCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC	3898
TTCTTGCGGC ACCGCCCACC AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG	3958
GCGCTGCCCT CCCCCACGGC CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCTC	4018
GGGCCGCTC CTCCAGAATC GAGAGGGCTG AGCCCCCTCT CTCTCGTCC GGCCTGCAGC	4078
ACAGAAGGGG GCCTCCCCGG GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCCTGC	4138
CCTGCACCTT GGGCACGGGA GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCGT	4198
GACCGGCCCC CCACCTTGTA CAGAACCAGC ACTCCAGGG CCCGAGCGCG TGCCTTCCCC	4258
GTGCGCAGCC GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC	4318
ACCTCCCGGT GTATGCAGTG GTGATGCCTA AAGGAATGTC ACG	4361

(2) INFORMATION FOR SEQ ID NO:24:

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## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 959 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	1	5	10	15
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	20	25	30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln	35	40	45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser	50	55	60	
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu	65	70	75	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro	85	90	95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	100	105	110	
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	115	120	125	
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	130	135	140	
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	145	150	155	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	165	170	175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	180	185	190	
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	195	200	205	
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	210	215	220	
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	225	230	235	
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	245	250	255	
Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	260	265	270	
Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	275	280	285	
Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	290	295	300	
Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu				

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305		310		315		320
Asn Ile Thr Asp	Pro 325	Pro Arg Gly Cys Val 330	Gly Asn Thr Asn Ile Trp 335			
Lys Thr Gly	Pro 340	Phe Lys Arg Val 345	Leu Met Ser Ser Lys Tyr Ala 350			
Asp Gly Val 355	Thr Gly Arg Val 360	Glu Phe Asn Glu Asp 365	Gly Asp Arg Lys			
Phe Ala Asn Tyr Ser Ile Met 375	Asn Leu Gln Asn Arg 380	Lys Leu Val Gln				
Val Gly Ile Tyr Asn 390	Gly Thr His Val Ile Pro 395	Asn Asp Arg Lys Ile 400				
Ile Trp Pro Gly Gly 405	Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser 415					
Thr Arg Leu Lys Ile Val Thr Ile His 425	Gln Glu Pro Phe Val Tyr Val 430					
Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn 445						
Gly Asp Pro Val Lys Lys Val 455	Ile Cys Thr Gly Pro Asn Asp Thr Ser 460					
Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys 480						
Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu 495						
Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn 510						
Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser 525						
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg 540						
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr 560						
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met 575						
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His 590						
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly 605						
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu 620						
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile 640						
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val 655						
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu						

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660					665					670					
Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile
	675						680					685			
Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr
	690					695					700				
Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu
705					710					715					720
Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala
				725					730					735	
Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp
			740					745					750		
Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val
		755					760					765			
Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg
	770					775					780				
Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser
785					790					795					800
His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr
				805					810					815	
Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu
			820					825					830		
Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly
		835					840					845			
Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala
	850					855					860				
Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg
865					870					875					880
Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys
				885					890					895	
Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe
			900					905					910		
Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg	Gly
	915						920					925			
Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	Glu
	930					935					940				
Arg	Glu	Glu	Gly	Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser	
945					950					955					

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

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## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2937

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG	867
Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	200
190 195	

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TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
	235				240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
		270						275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
	300					305					310					
GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
	315				320					325					330	
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
				335			340							345		
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
			350				355						360			
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
		365					370					375				
GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
	380					385					390					
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
				400						405					410	
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415				420						425		
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
			430				435					440				
GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	1635
Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	
		445					450					455				
CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	1683
Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	
	460					465					470					

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GAG Glu 475	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile 480	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro 485	TTC Phe	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 490	1731
CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val 495	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro 500	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp 505	TCG Ser	1779
TTC Phe	ATG Met	CAG Gln 510	CCG Pro	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu 515	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly 520	CTG Leu	TCG Ser	1827
GTG Val	CAC His 525	GTG Val	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu 530	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg 535	TTC Phe	AGC Ser	CCC Pro	1875
TTC Phe 540	GGC Gly	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn 545	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala	CTG Leu	1923
ACC Thr 555	CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met 560	TGG Trp	TTC Phe	TCC Ser	TGG Trp	GGC Gly 565	GTC Val	CTG Leu	CTC Leu	AAC Asn	TCC Ser 570	1971
GGC Gly	ATC Ile	GGG Gly	GAA Glu	GGC Gly 575	GCC Ala	CCC Pro	AGA Arg	AGC Ser	TTC Phe 580	TCA Ser	GCG Ala	CGC Arg	ATC Ile	CTG Leu 585	GGC Gly	2019
ATG Met	GTG Val	TGG Trp	GCC Ala 590	GGC Gly	TTT Phe	GCC Ala	ATG Met	ATC Ile 595	ATC Ile	GTG Val	GCC Ala	TCC Ser	TAC Tyr 600	ACC Thr	GCC Ala	2067
AAC Asn	CTG Leu 605	GCG Ala	GCC Ala	TTC Phe	CTG Leu	GTG Val	CTG Leu 610	GAC Asp	CGG Arg	CCG Pro	GAG Glu	GAG Glu	CGC Arg	ATC Ile	ACG Thr	2115
GGC Gly 620	ATC Ile	AAC Asn	GAC Asp	CCT Pro	CGG Arg	CTG Leu 625	AGG Arg	AAC Asn	CCC Pro	TCG Ser	GAC Asp 630	AAG Lys	TTT Phe	ATC Ile	TAC Tyr	2163
GCC Ala 635	ACG Thr	GTG Val	AAG Lys	CAG Gln	AGC Ser 640	TCC Ser	GTG Val	GAT Asp	ATC Ile	TAC Tyr 645	TTC Phe	CGG Arg	CGC Arg	CAG Gln	GTG Val 650	2211
GAG Glu	CTG Leu	AGC Ser	ACC Thr	ATG Met 655	TAC Tyr	CGG Arg	CAT His	ATG Met	GAG Glu 660	AAG Lys	CAC His	AAC Asn	TAC Tyr	GAG Glu 665	AGT Ser	2259
GCG Ala	GCG Ala	GAG Glu	GCC Ala 670	ATC Ile	CAG Gln	GCC Ala	GTG Val	AGA Arg 675	GAC Asp	AAC Asn	AAG Lys	CTG Leu	CAT His 680	GCC Ala	TTC Phe	2307
ATC Ile	TGG Trp	GAC Asp 685	TCG Ser	GCG Ala	GTG Val	CTG Leu	GAG Glu 690	TTC Phe	GAG Glu	GCC Ala	TCG Ser	CAG Gln 695	AAG Lys	TGC Cys	GAC Asp	2355
CTG Leu 700	GTG Val	ACG Thr	ACT Thr	GGA Gly	GAG Glu	CTG Leu 705	TTT Phe	TTC Phe	CGC Arg	TCG Ser	GGC Gly 710	TTC Phe	GGC Gly	ATA Ile	GGC Gly	2403
ATG Met 715	CGC Arg	AAA Lys	GAC Asp	AGC Ser	CCC Pro 720	TGG Trp	AAG Lys	CAG Gln	AAC Asn	GTC Val 725	TCC Ser	CTG Leu	TCC Ser	ATC Ile	CTC Leu 730	2451
AAG Lys	TCC Ser	CAC His	GAG Glu	AAT Asn 735	GGC Gly	TTC Phe	ATG Met	GAA Glu	GAC Asp 740	CTG Leu	GAC Asp	AAG Lys	ACG Thr	TGG Trp 745	GTT Val	2499



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CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT	2547
Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr	
750 755 760	
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG	2595
Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val	
765 770 775	
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG	2643
Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys	
780 785 790	
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG	2691
Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val	
795 800 805 810	
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC	2739
Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp	
815 820 825	
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC	2787
Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser	
830 835 840	
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA	2835
Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly	
845 850 855	
CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT	2883
Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala	
860 865 870	
ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG	2931
Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu	
875 880 885 890	
AGC TGAGACTCCC CGCCCCCCTT CCTCTGCCCC CTCCCCCGCA GACAGACAGA	2984
Ser	
CAGACGGACG GGACAGCGGC CCGGCCACG CAGAGCCCCG GAGCACCACG GGGTCGGGGG	3044
AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC	3104
GGTCCACCCC GTCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT	3164
GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC	3224
AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCACCTG CCCAGTTAGC	3284
CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC	3344
CCAGAGACTG CCCACCTGG GCCTCCCGTC CGTCCGCCCC CCCACCCCGC TGCTTGGCGG	3404
GCAGCCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC	3464
GGCTGGGCAG GGCCCGAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG	3524
GGGAGCGGGG GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC	3584
CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCCATGG CCCCAGCTGG CTGGGTGCGC	3644
CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCGGC	3704
ACCGCCACC AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT	3764
CCCCACGGC CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CCGCCGCCTC GGGCCGCCTC	3824

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CTCCAGAATC GAGAGGGCTG AGCCCCCTCCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG	3884
GCCTCCCCCG GGGTCCCCCG ACGCTGGCTC GGGACTGTCT TCAACCCTGC CCTGCACCTT	3944
GGGCACGGGA GAGCGCCACC CGCCCGCCCC CGCCCTCGCT CCGGGTGCCT GACCGGCCCCG	4004
CCACCTTGTA CAGAACCAGC ACTCCCAGGG CCGAGCGCG TGCCTTCCCC GTGCGCAGCC	4064
GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT	4124
GTATGCAGTG GTGATGCCTA AAGGAATGTC ACG	4157

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 891 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	1	5	10	15
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	20	25	30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln	35	40	45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser	50	55	60	
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu	65	70	75	80
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro	85	90	95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	100	105	110	
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	115	120	125	
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	130	135	140	
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	145	150	155	160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	165	170	175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	180	185	190	
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	195	200	205	
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	210	215	220	
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile				

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225		230		235		240									
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala
				245					250					255	
Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro
			260					265					270		
Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr
		275					280					285			
Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr
	290					295					300				
Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr
305					310					315					320
Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly
				325					330					335	
Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys
			340					345					350		
Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu
		355					360					365			
Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val
	370					375					380				
Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro
385					390					395					400
Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu
				405					410					415	
Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val
			420					425					430		
Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys
			435				440					445			
Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp
	450					455					460				
Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile
465					470					475					480
Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys
				485					490					495	
Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln
			500					505					510		
Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val
							520					525			
Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val
	530					535					540				
Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met
545					550					555					560
Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala
				565					570					575	
Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe

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580					585					590				
Ala Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu
	595					600					605			
Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro
	610					615					620			
Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln
	625					630					635			640
Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met
				645					650					655
Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile
				660					665					670
Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala
				675					680					685
Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly
				690					695					700
Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser
				705					710					720
Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn
				725					730					735
Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys
				740					745					750
Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala
				755					760					765
Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu
				770					775					780
Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys
				785					790					800
Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu
				805					810					815
Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala
				820					825					830
Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg
				835					840					845
Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln
				850					855					860
Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Gly
				865					870					880
Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser				
				885					890					

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3794 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both

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(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAAGCCGGGC GTTCGGAGCT GTGCCC GGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCG CAGCC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819

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His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
235					240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
			270					275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
	300					305					310					
GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
315					320					325					330	
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
				335					340					345		
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
			350					355					360			
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
		365					370					375				
GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
	380					385					390					
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
				400						405					410	
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415					420					425		
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
			430					435					440			

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GTG Val	AAC Asn	AAC Asn 445	AGC Ser	AAC Asn	AAG Lys	AAG Lys	GAG Glu 450	TGG Trp	AAT Asn	GGG Gly	ATG Met 455	ATG Met	GGC Gly	GAG Glu	CTG Leu	1635
CTC Leu	AGC Ser 460	GGG Gly	CAG Gln	GCA Ala	GAC Asp	ATG Met 465	ATC Ile	GTG Val	GCG Ala	CCG Pro	CTA Leu 470	ACC Thr	ATA Ile	AAC Asn	AAC Asn	1683
GAG Glu 475	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile 480	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro 485	TTC Phe	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 490	1731
CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val 495	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro 500	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp 505	TCG Ser	1779
TTC Phe	ATG Met	CAG Gln 510	CCG Pro	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu 515	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly 520	CTG Leu	TCG Ser	1827
GTG Val	CAC His 525	GTG Val	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu 530	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg 535	TTC Phe	AGC Ser	CCC Pro	1875
TTC Phe 540	GGC Gly	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn 545	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala	CTG Leu	1923
ACC Thr 555	CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met 560	TGG Trp	TTC Phe	TCC Ser	TGG Trp	GGC Gly 565	GTC Val	CTG Leu	CTC Leu	AAC Asn	TCC Ser 570	1971
GGC Gly	ATC Ile	GGG Gly	GAA Glu	GGC Gly 575	GCC Ala	CCC Pro	AGA Arg	AGC Ser	TTC Phe 580	TCA Ser	GCG Ala	CGC Arg	ATC Ile	CTG Leu 585	GGC Gly	2019
ATG Met	GTG Val	TGG Trp	GCC Ala 590	GGC Gly	TTT Phe	GCC Ala	ATG Met	ATC Ile 595	ATC Ile	GTG Val	GCC Ala	TCC Ser	TAC Tyr 600	ACC Thr	GCC Ala	2067
AAC Asn	CTG Leu 605	GCG Ala	GCC Ala	TTC Phe	CTG Leu	GTG Val	CTG Leu	GAC Asp 610	CGG Arg	CCG Pro	GAG Glu 615	GAG Glu	CGC Arg	ATC Ile	ACG Thr	2115
GGC Gly 620	ATC Ile	AAC Asn	GAC Asp	CCT Pro	CGG Arg	CTG Leu 625	AGG Arg	AAC Asn	CCC Pro	TCG Ser	GAC Asp 630	AAG Lys	TTT Phe	ATC Ile	TAC Tyr	2163
GCC Ala 635	ACG Thr	GTG Val	AAG Lys	CAG Gln	AGC Ser 640	TCC Ser	GTG Val	GAT Asp	ATC Ile	TAC Tyr 645	TTC Phe	CGG Arg	CGC Arg	CAG Gln	GTG Val 650	2211
GAG Glu	CTG Leu	AGC Ser	ACC Thr	ATG Met 655	TAC Tyr	CGG Arg	CAT His	ATG Met	GAG Glu 660	AAG Lys	CAC His	AAC Asn	TAC Tyr	GAG Glu 665	AGT Ser	2259
GCG Ala	GCG Ala	GAG Glu	GCC Ala 670	ATC Ile	CAG Gln	GCC Ala	GTG Val	AGA Arg 675	GAC Asp	AAC Asn	AAG Lys	CTG Leu	CAT His 680	GCC Ala	TTC Phe	2307
ATC Ile	TGG Trp	GAC Asp 685	TCG Ser	GCG Ala	GTG Val	CTG Leu	GAG Glu 690	TTC Phe	GAG Glu	GCC Ala	TCG Ser	CAG Gln	AAG Lys	TGC Cys	GAC Asp	2355
CTG Leu 700	GTG Val	ACG Thr	ACT Thr	GGA Gly	GAG Glu	CTG Leu 705	TTT Phe	TTC Phe	CGC Arg	TCG Ser	GGC Gly 710	TTC Phe	GGC Gly	ATA Ile	GGC Gly	2403

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ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC	2451
Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu	
715 720 725 730	
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT	2499
Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val	
735 740 745	
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT	2547
Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr	
750 755 760	
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG	2595
Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val	
765 770 775	
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG	2643
Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys	
780 785 790	
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG	2691
Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val	
795 800 805 810	
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC	2739
Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp	
815 820 825	
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC	2787
Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser	
830 835 840	
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT	2835
Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr	
845 850 855	
GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG	2883
Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val	
860 865 870	
GTG TGAGGCCCCC GGAGGCGCCC ACCTGCCCCAG TTAGCCCGGC CAAGGACACT	2936
Val	
875	
GATGGGTCCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCCAC	2996
CCTGGGCCTC CCGTCCGTCC GCCCGCCCAC CCCGCTGCCT GGCGGGCAGC CCCTGCTGGA	3056
CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG GGCAGGGCCG	3116
CAGGGCGCTC CGGCAGAGGC AGGCCCCCTGG GGTCTCTGAG CAGTGGGGAG CGGGGGCTAA	3176
CTGCCCCCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC CGCAGCACCA	3236
GCCTGAGCCA CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCGCCCCCTCC TCGGGCGCCT	3296
GCGCTCCTCT GCAGCCTGAG CTCCACCCTC CCCTCTTCTT GCGGCACCGC CCACCAAACA	3356
CCCCGTCTGC CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC ACGGCCGTCC	3416
CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA GAATCGAGAG	3476
GGCTGAGCCC CTCCTCTCCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC CCCGGGGGTC	3536
CCCGGACGCT GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA CGGGAGAGCG	3596
CCACCCGCCC GCCCCGCCC TCGCTCCGGG TGCGTGACCG GCCCGCCACC TTGTACAGAA	3656



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CCAGCACTCC	CAGGGCCCGA	GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	CTGCCCCCTCC	3716
GTCCCCAGGG	TGCAGGCGCG	CACCGCCCAA	CCCCCACCTC	CCGGTGTATG	CAGTGGTGAT	3776
GCCTAAAGGA	ATGTCACG					3794

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 875 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met 1	Ser	Thr	Met	Arg 5	Leu	Leu	Thr	Leu	Ala 10	Leu	Leu	Phe	Ser	Cys 15	Ser
Val	Ala	Arg	Ala 20	Ala	Cys	Asp	Pro	Lys 25	Ile	Val	Asn	Ile	Gly 30	Ala	Val
Leu	Ser	Thr 35	Arg	Lys	His	Glu	Gln 40	Met	Phe	Arg	Glu	Ala 45	Val	Asn	Gln
Ala	Asn 50	Lys	Arg	His	Gly	Ser 55	Trp	Lys	Ile	Gln	Leu 60	Asn	Ala	Thr	Ser
Val 65	Thr	His	Lys	Pro	Asn 70	Ala	Ile	Gln	Met	Ala 75	Leu	Ser	Val	Cys	Glu 80
Asp	Leu	Ile	Ser	Ser 85	Gln	Val	Tyr	Ala	Ile 90	Leu	Val	Ser	His	Pro 95	Pro
Thr	Pro	Asn 100	Asp	His	Phe	Thr	Pro	Thr 105	Pro	Val	Ser	Tyr	Thr 110	Ala	Gly
Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr	Thr	Arg	Met 125	Ser	Ile	Tyr
Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu	Arg	Thr 140	Val	Pro	Pro	Tyr
Ser 145	His	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met	Met 155	Arg	Val	Tyr	Ser	Trp 160
Asn	His	Ile	Ile	Leu 165	Leu	Val	Ser	Asp	Asp 170	His	Glu	Gly	Arg	Ala 175	Ala
Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu 185	Glu	Arg	Glu	Ser	Lys 190	Ser	Lys
Lys	Arg	Asn 195	Tyr	Glu	Asn	Leu	Asp 200	Gln	Leu	Ser	Tyr	Asp 205	Asn	Lys	Arg
Gly	Pro 210	Lys	Ala	Glu	Lys	Val 215	Leu	Gln	Phe	Asp	Pro 220	Gly	Thr	Lys	Asn
Val 225	Thr	Ala	Leu	Leu	Met 230	Glu	Ala	Lys	Glu	Leu 235	Glu	Ala	Arg	Val	Ile 240
Ile	Leu	Ser	Ala	Ser 245	Glu	Asp	Asp	Ala	Ala 250	Thr	Val	Tyr	Arg	Ala 255	Ala
Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro

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260					265					270					
Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr
		275					280					285			
Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr
	290					295					300				
Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr
305				310					315					320	
Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly
			325						330					335	
Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys
			340					345					350		
Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu
		355					360					365			
Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val
	370					375					380				
Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro
385				390					395						400
Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu
			405						410					415	
Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val
		420						425					430		
Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys
		435					440					445			
Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp
	450					455					460				
Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile
465				470					475					480	
Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys
			485						490					495	
Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln
			500					505					510		
Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val
		515					520					525			
Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val
	530					535					540				
Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met
545				550							555				560
Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala
			565						570					575	
Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe
			580					585					590		
Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu
		595					600					605			
Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg
	610					615						620			

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Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser
625					630					635					640
Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr
				645					650					655	
Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln
			660					665						670	
Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val
			675				680					685			
Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu
	690					695					700				
Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro
705					710					715					720
Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly
				725					730					735	
Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp
			740					745					750		
Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly
			755				760					765			
Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile
	770					775					780				
Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln
785					790					795					800
Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln
				805					810					815	
Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr
			820					825						830	
Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg
			835				840					845			
Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro	Leu
			850			855					860				
Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val					
865					870					875					

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4094 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45 50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60 65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75 80	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95 100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110 115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125 130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140 145	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	170
155 160	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	185
175 180	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	200
190 195	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	215
205 210	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA	963
Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	230
220 225	

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GCC Ala 235	GCG Ala	ATG Met	CTG Leu	AAC Asn 240	ATG Met	ACG Thr	GGC Gly	AAC Asn	ACC Thr	AAC Asn 245	ATC Ile	TGG Trp	AAG Lys	ACC Thr	GGG Gly 250	1011
CCG Pro	CTC Leu	TTC Phe	AAG Lys 255	AGA Arg	GTG Val	CTG Leu	ATG Met	TCT Ser	TCC Ser	AAG Lys	TAT Tyr	GCG Ala	GAT Asp	GGG Gly 265	GTG Val	1059
ACT Thr	GGT Gly	CGC Arg	GTG Val 270	GAG Glu	TTC Phe	AAT Asn	GAG Glu	GAT Asp 275	GGG Gly	GAC Asp	CGG Arg	AAG Lys	TTC Phe 280	GCC Ala	AAC Asn	1107
TAC Tyr	AGC Ser	ATC Ile 285	ATG Met	AAC Asn	CTG Leu	CAG Gln	AAC Asn 290	CGC Arg	AAG Lys	CTG Leu	GTG Val	CAA Gln 295	GTG Val	GGC Gly	ATC Ile	1155
TAC Tyr 300	AAT Asn	GGC Gly	ACC Thr	CAC His	GTC Val	ATC Ile 305	CCT Pro	AAT Asn	GAC Asp	AGG Arg	AAG Lys 310	ATC Ile	ATC Ile	TGG Trp	CCA Pro	1203
GGC Gly 315	GGA Gly	GAG Glu	ACA Thr	GAG Glu	AAG Lys 320	CCT Pro	CGA Arg	GGG Gly	TAC Tyr	CAG Gln 325	ATG Met	TCC Ser	ACC Thr	AGA Arg	CTG Leu 330	1251
AAG Lys	ATT Ile	GTG Val	ACG Thr	ATC Ile 335	CAC His	CAG Gln	GAG Glu	CCC Pro	TTC Phe 340	GTG Val	TAC Tyr	GTC Val	AAG Lys	CCC Pro 345	ACG Thr	1299
CTG Leu	AGT Ser	GAT Asp	GGG Gly 350	ACA Thr	TGC Cys	AAG Lys	GAG Glu	GAG Glu 355	TTC Phe	ACA Thr	GTC Val	AAC Asn	GGC Gly 360	GAC Asp	CCA Pro	1347
GTC Val	AAG Lys 365	AAG Lys	GTG Val	ATC Ile	TGC Cys	ACC Thr	GGG Gly 370	CCC Pro	AAC Asn	GAC Asp	ACG Thr	TCG Ser 375	CCG Pro	GGC Gly	AGC Ser	1395
CCC Pro 380	CGC Arg	CAC His	ACG Thr	GTG Val	CCT Pro	CAG Gln 385	TGT Cys	TGC Cys	TAC Tyr	GGC Gly 390	TTT Phe	TGC Cys	ATC Ile	GAC Asp	CTG Leu	1443
CTC Leu 395	ATC Ile	AAG Lys	CTG Leu	GCA Ala 400	CGG Arg	ACC Thr	ATG Met	AAC Asn	TTC Phe 405	ACC Thr	TAC Tyr	GAG Glu	GTG Val	CAC His	CTG Leu 410	1491
GTG Val	GCA Ala	GAT Asp	GGC Gly 415	AAG Lys	TTC Phe	GGC Gly	ACA Thr	CAG Gln 420	GAG Glu	CGG Arg	GTG Val	AAC Asn	AAC Asn	AGC Ser 425	AAC Asn	1539
AAG Lys	AAG Lys	GAG Glu	TGG Trp 430	AAT Asn	GGG Gly	ATG Met	ATG Met	GGC Gly 435	GAG Glu	CTG Leu	CTC Leu	AGC Ser	GGG Gly 440	CAG Gln	GCA Ala	1587
GAC Asp	ATG Met	ATC Ile 445	GTG Val	GCG Ala	CCG Pro	CTA Leu	ACC Thr 450	ATA Ile	AAC Asn	AAC Asn	GAG Glu	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	1635
ATC Ile 460	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro	TTC Phe 465	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 470	CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val	1683
AAG Lys 475	AAG Lys	GAG Glu	ATT Ile	CCC Pro	CGG Arg 480	AGC Ser	ACG Thr	CTG Leu	GAC Asp	TCG Ser 485	TTC Phe	ATG Met	CAG Gln	CCG Pro	TTC Phe 490	1731
CAG Gln	AGC Ser	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val	CAC His	GTG Val	GTG Val	GCC Ala	1779



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Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	
765						770				775						
CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG	2643
Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	
780						785				790						
CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	2691
Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	
795				800						805				810		
ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	TTC	AAG	AGG	CGT	2739
Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	
				815				820						825		
AGG	TCC	TCC	AAA	GAC	ACG	AGC	ACC	GGG	GGT	GGA	CGC	GGT	GCT	TTG	CAA	2787
Arg	Ser	Ser	Lys	Asp	Thr	Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln	
		830						835				840				
AAC	CAA	AAA	GAC	ACA	GTG	CTG	CCG	CGA	CGC	GCT	ATT	GAG	AGG	GAG	GAG	2835
Asn	Gln	Lys	Asp	Thr	Val	Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu	
		845				850						855				
GGC	CAG	CTG	CAG	CTG	TGT	TCC	CGT	CAT	AGG	GAG	AGC	TGAGACTCCC				2881
Gly	Gln	Leu	Gln	Leu	Cys	Ser	Arg	His	Arg	Glu	Ser					
860						865				870						
CGCCCCGCCCT				CCTCTGCCCC			CTCCCCCGCA		GACAGACAGA			CAGACGGACG		GGACAGCGGC		2941
CCGGCCCACG				CAGAGCCCCG			GAGCACCACG		GGGTCGGGGG			AGGAGCACCC		CCAGCCTCCC		3001
CCAGGCTGCG				CCTGCCCCGCC			CGCCGGTTGG		CCGGCTGGCC			GGTCCACCCC		GTCCCGGCCC		3061
CGCGCGTGCC				CCCAGCGTGG			GGCTAACGGG		CGCCTTGTCT			GTGTATTTCT		ATTTTGCAGC		3121
AGTACCATCC				CACTGATATC			ACGGGCCCCG		TCAACCTCTC			AGATCCCTCG		GTCAGCACCG		3181
TGGTGTGAGG				CCCCCGGAGG			CGCCCACCTG		CCCAGTTAGC			CCGGCCAAGG		ACACTGATGG		3241
GTCCTGCTGC				TCGGGAAGGC			CTGAGGGAAG		CCCACCCGCC			CCAGAGACTG		CCCACCCTGG		3301
GCCTCCCGTC				CGTCCGCCCC			CCCACCCCGC		TGCCTGGCGG			GCAGCCCCTG		CTGGACCAAG		3361
GTGCGGACCG				GAGCGGCTGA			GGACGGGGCA		GAGCTGAGTC			GGCTGGGCAG		GGCCGCAGGG		3421
CGCTCCGGCA				GAGGCAGGCC												

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 870 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met 1	Ser	Thr	Met	Arg 5	Leu	Leu	Thr	Leu	Ala 10	Leu	Leu	Phe	Ser	Cys 15	Ser
Val	Ala	Arg	Ala 20	Ala	Cys	Asp	Pro	Lys 25	Ile	Val	Asn	Ile	Gly 30	Ala	Val
Leu	Ser	Thr 35	Arg	Lys	His	Glu	Gln 40	Met	Phe	Arg	Glu	Ala 45	Val	Asn	Gln
Ala	Asn 50	Lys	Arg	His	Gly	Ser 55	Trp	Lys	Ile	Gln	Leu 60	Asn	Ala	Thr	Ser
Val 65	Thr	His	Lys	Pro	Asn 70	Ala	Ile	Gln	Met	Ala 75	Leu	Ser	Val	Cys	Glu 80
Asp	Leu	Ile	Ser	Ser 85	Gln	Val	Tyr	Ala	Ile 90	Leu	Val	Ser	His	Pro 95	Pro
Thr	Pro	Asn 100	Asp	His	Phe	Thr	Pro	Thr 105	Pro	Val	Ser	Tyr	Thr 110	Ala	Gly
Phe	Tyr	Arg 115	Ile	Pro	Val	Leu	Gly 120	Leu	Thr	Thr	Arg	Met 125	Ser	Ile	Tyr
Ser	Asp 130	Lys	Ser	Ile	His	Leu 135	Ser	Phe	Leu	Arg	Thr 140	Val	Pro	Pro	Tyr
Ser 145	His	Gln	Ser	Ser	Val 150	Trp	Phe	Glu	Met	Met 155	Arg	Val	Tyr	Ser	Trp 160
Asn	His	Ile	Ile	Leu 165	Leu	Val	Ser	Asp	Asp 170	His	Glu	Gly	Arg	Ala 175	Ala
Gln	Lys	Arg	Leu 180	Glu	Thr	Leu	Leu	Glu 185	Glu	Arg	Glu	Ser	Lys 190	Ala	Glu
Lys	Val	Leu 195	Gln	Phe	Asp	Pro	Gly 200	Thr	Lys	Asn	Val	Thr 205	Ala	Leu	Leu
Met	Glu 210	Ala	Lys	Glu	Leu	Glu 215	Ala	Arg	Val	Ile	Ile 220	Leu	Ser	Ala	Ser
Glu 225	Asp	Asp	Ala	Ala	Thr 230	Val	Tyr	Arg	Ala	Ala 235	Ala	Met	Leu	Asn	Met 240
Thr	Gly	Asn	Thr	Asn 245	Ile	Trp	Lys	Thr	Gly 250	Pro	Leu	Phe	Lys	Arg 255	Val
Leu	Met	Ser	Ser 260	Lys	Tyr	Ala	Asp	Gly 265	Val	Thr	Gly	Arg	Val 270	Glu	Phe
Asn	Glu 275	Asp	Gly	Asp	Arg	Lys	Phe 280	Ala	Asn	Tyr	Ser	Ile 285	Met	Asn	Leu



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Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val  
 290 295 300  
 Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys  
 305 310 315 320  
 Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His  
 325 330 335  
 Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys  
 340 345 350  
 Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys  
 355 360 365  
 Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro  
 370 375 380  
 Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg  
 385 390 395 400  
 Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe  
 405 410 415  
 Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly  
 420 425 430  
 Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro  
 435 440 445  
 Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro  
 450 455 460  
 Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg  
 465 470 475 480  
 Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu  
 485 490 495  
 Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu  
 500 505 510  
 Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu  
 515 520 525  
 Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly  
 530 535 540  
 Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser  
 545 550 555 560  
 Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val  
 565 570 575  
 Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro  
 580 585 590  
 Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser  
 595 600 605  
 Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr  
 610 615 620  
 Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys  
 625 630 635 640  
 His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn

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645					650					655					
Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala
			660					665					670		
Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser
		675					680					685			
Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val
	690					695					700				
Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu
	705					710					715				720
Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala
				725					730					735	
Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val
			740					745					750		
Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala
		755					760					765			
Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe
	770					775					780				
Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly
	785					790					795				800
Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr
			805						810					815	
Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr
		820						825					830		
Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val
		835				840						845			
Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu	Gly	Gln	Leu	Gln	Leu	Cys
	850					855					860				
Ser	Arg	His	Arg	Glu	Ser										
	865					870									

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 262..2826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120

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CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCGG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala 1 5 10	291
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 15 20 25	339
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 30 35 40	387
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 45 50 55	435
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 60 65 70	483
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 75 80 85 90	531
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 95 100 105	579
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 110 115 120	627
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 125 130 135	675
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190 195 200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011

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CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	1059
Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	
				255					260					265		
ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	1107
Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	
			270					275					280			
TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	1155
Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	
		285					290					295				
TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	1203
Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	
	300					305					310					
GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	1251
Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	
315					320					325					330	
AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	1299
Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	
				335					340					345		
CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	1347
Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	
			350					355					360			
GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	1395
Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	
		365					370					375				
CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	1443
Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	
	380					385					390					
CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	1491
Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	
395					400				405					410		
GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	1539
Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	
				415				420						425		
AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	1587
Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	
			430					435					440			
GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	1635
Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	
		445					450					455				
ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	1683
Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	
	460					465					470					
AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	1731
Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	
475					480					485					490	
CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	1779
Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	
				495				500						505		
GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	1827
Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	

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			510				515				520							
GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	1875		
Val	Asn	Ser	Glu	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala			
		525					530					535						
ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	1923		
Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly			
	540					545					550							
GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	1971		
Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly			
555					560					565					570			
TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	2019		
Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe			
				575					580					585				
CTG	GTG	CTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	2067		
Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro			
			590					595					600					
CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	2115		
Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln			
		605					610					615						
AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	2163		
Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met			
	620					625					630							
TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	2211		
Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile			
635					640					645					650			
CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	2259		
Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala			
				655					660					665				
GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	2307		
Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly			
			670					675					680					
GAG	CTG	TTT	TTC	CGC	TCG	GGC	TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	2355		
Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser			
		685					690					695						
CCC	TGG	AAG	CAG	AAC	GTC	TCC	CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	2403		
Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn			
	700					705					710							
GGC	TTC	ATG	GAA	GAC	CTG	GAC	AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	2451		
Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys			
715					720				725						730			
GAC	TCG	CGC	AGC	AAC	GCC	CCT	GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	2499		
Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala			
				735					740					745				
GGG	GTC	TTC	ATG	CTG	GTA	GCT	GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	2547		
Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu			
			750					755					760					
ATT	TTC	ATC	GAG	ATT	GCC	TAC	AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	2595		
Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys			
		765					770					775						
CAG	ATG	CAG	CTG	GCC	TTT	GCC	GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG	2643		

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Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	
	780					785					790					
CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	2691
Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	
795					800					805					810	
ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	TTC	AAG	AGG	CGT	2739
Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	
				815					820					825		
AGG	TCC	TCC	AAA	GAC	ACG	CAG	TAC	CAT	CCC	ACT	GAT	ATC	ACG	GGC	CCG	2787
Arg	Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro	
			830					835					840			
CTC	AAC	CTC	TCA	GAT	CCC	TCG	GTC	AGC	ACC	GTG	GTG	TGAGG	CCCCC			2833
Leu	Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val					
		845					850					855				
GGAGGCGCCC	ACCTGCCCAG	TTAGCCC	GGC	CAAGGACACT	GATGGGTCCT	GCTGCTCGGG										2893
AAGGCTGAG	GGAAGCCCAC	CCGCCCCAGA	GACTGCCCAC	CCTGGGCCTC	CCGTCCGTCC											2953
GCCCCGCCAC	CCCCTGCTCT	GGCGGGCAGC	CCCTGCTGGA	CCAAGGTGCG	GACCGGAGCG											3013
GCTGAGGACG	GGGCAGAGCT	GAGTCGGCTG	GGCAGGGCCG	CAGGGCGCTC	CGGCAGAGGC											3073
AGGCCCCCTGG	GGTCTCTGAG	CAGTGGGGAG	CGGGGGCTAA	CTGCCCCCAG	GCGGAGGGGC											3133
TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	CGCAGCACCA	GCCTGAGCCA	CAGTGGGGCC											3193
CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTC	TCGGGCGCCT	GCGCTCCTCT	GCAGCCTGAG											3253
CTCCACCCTC	CCCTCTTCTT	GCGGCACCGC	CCACCAAACA	CCCCGTCTGC	CCCTTGACGC											3313
CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	ACGGCCGTCC	CTGACTTCCC	AGCTGGCAGC											3373
GCCTCCCGCC	GCCTCGGGCC	GCCTCCTCCA	GAATCGAGAG	GGCTGAGCCC	CTCCTCTCCT											3433
CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	CCCGGGGGTC	CCCGGACGCT	GGCTCGGGAC											3493
TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	CGGGAGAGCG	CCACCCGCCC	GCCCCCGCCC											3553
TCGCTCCGGG	TGCGTGACCG	GCCCGCCACC	TTGTACAGAA	CCAGCACTCC	CAGGGCCCCGA											3613
GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	CTGCCCCTCC	GTCCCCAGGG	TGCAGGCGCG											3673
CACCGCCCCA	CCCCCACCTC	CCGGTGTATG	CAGTGGTGAT	GCCTAAAGGA	ATGTCACG											3731

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 854 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	
1				5					10					15		
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	
			20					25					30			

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Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
225 230 235 240

Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val  
245 250 255

Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe  
260 265 270

Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu  
275 280 285

Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val  
290 295 300

Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys  
305 310 315 320

Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His  
325 330 335

Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys  
340 345 350

Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys  
355 360 365

Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro  
370 375 380

Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg

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385		390		395		400
Thr Met Asn Phe	Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe					
	405			410		415
Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly						
	420		425			430
Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro						
	435		440			445
Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro						
	450		455			460
Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg						
	465		470		475	480
Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu						
	485			490		495
Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu						
	500		505			510
Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu						
	515		520			525
Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly						
	530		535			540
Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser						
	545		550		555	560
Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val						
	565			570		575
Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro						
	580		585			590
Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser						
	595		600			605
Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr						
	610		615			620
Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys						
	625		630		635	640
His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn						
	645			650		655
Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala						
	660		665			670
Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser						
	675		680			685
Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val						
	690		695			700
Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu						
	705		710		715	720
Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala						
	725			730		735
Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val						



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740		745		750
Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala	755	760		765
Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe	770	775		780
Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly	785	790	795	800
Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr	805	810		815
Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr	820	825		830
Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro	835	840	845	
Ser Val Ser Thr Val Val	850			

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3007 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2988

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGCCGGGC GTTCGGAGCT GTGCCCCGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GC GCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	1 5 10
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	15 20 25
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	30 35 40
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	45 50 55

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CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
60						65				70						
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
75				80					85						90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	GAC	CCA	GGG	ACC	AAG	867
Arg	Glu	Ser	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	
			190					195					200			
AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	CTG	GAG	GCC	CGG	GTC	915
Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	
		205				210						215				
ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	ACT	GTA	TAC	CGC	GCA	963
Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	
		220				225					230					
GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	1011
Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	
235					240					245					250	
CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	1059
Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	
				255					260					265		
ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	1107
Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	
			270					275					280			
TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	1155
Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	
			285				290					295				
TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	1203
Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	
			300			305					310					
GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	1251
Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	
315					320					325					330	

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AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG	1299
Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr	
335 340 345	
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA	1347
Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro	
350 355 360	
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC	1395
Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser	
365 370 375	
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG	1443
Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu	
380 385 390	
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG	1491
Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu	
395 400 405 410	
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC	1539
Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn	
415 420 425	
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA	1587
Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala	
430 435 440	
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC	1635
Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr	
445 450 455	
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC	1683
Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val	
460 465 470	
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC	1731
Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe	
475 480 485 490	
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC	1779
Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala	
495 500 505	
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG	1827
Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys	
510 515 520	
GTG AAC AGC GAG GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC	1875
Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala	
525 530 535	
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC	1923
Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly	
540 545 550	
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC	1971
Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly	
555 560 565 570	
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC	2019
Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe	
575 580 585	
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT	2067
Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro	
590 595 600	

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CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605 610 615	2115
AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620 625 630	2163
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635 640 645 650	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655 660 665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670 675 680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685 690 695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700 705 710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715 720 725 730	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735 740 745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750 755 760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys 765 770 775	2595
CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu 780 785 790	2643
CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala 795 800 805 810	2691
ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg 815 820 825	2739
AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro 830 835 840	2787
GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu 845 850 855	2835
CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg 860 865 870	2883

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GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT	2931
Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg	
875 880 885 890	
CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG	2979
Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met	
895 900 905	
CAG TGG TGATGCCTAA AGGAATGTCA CG	3007
Gln Trp	

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 908 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser	1	5	10	15
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val	20	25	30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln	35	40	45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser	50	55	60	
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu	65	70	75	80
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro	85	90	95	
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly	100	105	110	
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr	115	120	125	
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr	130	135	140	
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp	145	150	155	160
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	165	170	175	
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Arg	Glu	Ser	Lys	Ala	Glu		180	185	190	
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	195	200	205	
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	210	215	220	
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met				

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225		230		235		240
Thr Gly Asn Thr	Asn Ile Trp Lys Thr Gly	Pro Leu Phe Lys Arg Val				
	245	250				255
Leu Met Ser Ser	Lys Tyr Ala Asp Gly	Val Thr Gly Arg Val Glu Phe				
	260	265				270
Asn Glu Asp Gly	Asp Arg Lys Phe Ala Asn Tyr Ser	Ile Met Asn Leu				
	275	280				285
Gln Asn Arg Lys	Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val					
	290	295				300
Ile Pro Asn Asp	Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys					
	305	310				315
Pro Arg Gly Tyr	Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His					
	325	330				335
Gln Glu Pro Phe	Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys					
	340	345				350
Lys Glu Glu Phe	Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys					
	355	360				365
Thr Gly Pro Asn	Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro					
	370	375				380
Gln Cys Cys Tyr	Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg					
	385	390				395
Thr Met Asn Phe	Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe					
	405	410				415
Gly Thr Gln Glu	Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly					
	420	425				430
Met Met Gly Glu	Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro					
	435	440				445
Leu Thr Ile Asn	Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro					
	450	455				460
Phe Lys Tyr Gln	Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg					
	465	470				475
Ser Thr Leu Asp	Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu					
	485	490				495
Leu Val Gly Leu	Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu					
	500	505				510
Asp Arg Phe Ser	Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu					
	515	520				525
Glu Glu Asp Ala	Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly					
	530	535				540
Val Leu Leu Asn	Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser					
	545	550				555
Ala Arg Ile Leu	Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val					
	565	570				575
Ala Ser Tyr Thr	Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro					
	580	585				590

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Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser  
 595 600 605  
 Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr  
 610 615 620  
 Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys  
 625 630 635 640  
 His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn  
 645 650 655  
 Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala  
 660 665 670  
 Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser  
 675 680 685  
 Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val  
 690 695 700  
 Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu  
 705 710 715 720  
 Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala  
 725 730 735  
 Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val  
 740 745 750  
 Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala  
 755 760 765  
 Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe  
 770 775 780  
 Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly  
 785 790 795 800  
 Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr  
 805 810 815  
 Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr  
 820 825 830  
 Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu  
 835 840 845  
 Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro  
 850 855 860  
 Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe  
 865 870 875 880  
 Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala  
 885 890 895  
 His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp  
 900 905

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 3998 base pairs  
 (B) TYPE: nucleic acid

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(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAAGCCGGGC GTTCGGAGCT GTGCCC GGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCGAGCC CGCGGGGGCCG GGCGAGCGCA	180
GGACGGCCCC GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15	
20	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30	
35	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	55
45	
50	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	70
60	
65	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	90
75	
80	
85	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	105
95	
100	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	120
110	
115	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	135
125	
130	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	150
140	
145	
150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Val Ser Asp Asp	170
155	
160	
165	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	



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175				180				185								
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
	235				240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
				255					260					265		
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
			270					275					280			
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
		285					290					295				
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
	300					305					310					
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
	315				320					325					330	
GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	1299
Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	
			335						340					345		
ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	1347
Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	
			350					355					360			
GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	1395
Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	
		365					370					375				
AAC	CGC	AAG	CTG	GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	1443
Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	
	380					385					390					
CCT	AAT	GAC	AGG	AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	1491
Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	
	395				400					405					410	
CGA	GGG	TAC	CAG	ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	1539
Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	
			415						420					425		
GAG	CCC	TTC	GTG	TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	1587
Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	
			430					435					440			
GAG	GAG	TTC	ACA	GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	1635

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Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	
		445					450					455				
GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	1683
Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	
	460					465					470					
TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	1731
Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	
475					480					485					490	
ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	1779
Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	
				495					500					505		
ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	1827
Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	
			510					515					520			
ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	1875
Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	
			525				530					535				
ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	1923
Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	
				540			545				550					
AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	1971
Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	
555					560					565					570	
ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	2019
Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	
				575					580					585		
GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	2067
Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	
				590				595					600			
CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	
			605				610					615				
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	
	620					625					630					
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
				640						645					650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660					665		
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
			670					675					680			
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
			685				690					695				
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
			700				705					710				

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CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883
GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln 910 915 920	3027
TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser 925 930 935	3075
GTC AGC ACC GTG GTG TGAGGCCCC GGAGGCGCCC ACCTGCCCAG TTAGCCCGGC Val Ser Thr Val Val 940	3130
CAAGGACACT GATGGGTCTT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA	3190
GACTGCCCAC CCTGGGCCTC CCGTCCGTCC GCCGCCCCAC CCCGCTGCCT GGCGGGCAGC	3250
CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG	3310
GGCAGGGCCG CAGGGCGCTC CGGCAGAGGC AGGCCCTGG GGTCTCTGAG CAGTGGGGAG	3370

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CGGGGGCTAA CTGCCCCCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC 3430  
 CGCAGCACCA GCCTGAGCCA CAGTGGGGCC CATGGCCCCA GCTGGCTGGG TCGCCCCTCC 3490  
 TCGGGCGCCT GCGCTCCTCT GCAGCCTGAG CTCCACCCTC CCCTCTTCTT GCGGCACCGC 3550  
 CCACCAAACA CCCCCTCTGC CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC 3610  
 ACGGCCGTCC CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA 3670  
 GAATCGAGAG GGCTGAGCCC CTCCTCTCCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC 3730  
 CCCGGGGGTC CCCGGACGCT GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA 3790  
 CGGGAGAGCG CCACCCGCCC GCCCCCGCCC TCGCTCCGGG TCGTGACCG GCCCGCCACC 3850  
 TTGTACAGAA CCAGCACTCC CAGGGCCCGA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT 3910  
 CTGCCCCTCC GTCCCCAGGG TGCAGGCGCG CACCGCCCAA CCCCACCTC CCGGTGTATG 3970  
 CAGTGGTGAT GCCTAAAGGA ATGTCACG 3998

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 943 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser  
 1 5 10 15  
 Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val  
 20 25 30  
 Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
 35 40 45  
 Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
 50 55 60  
 Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
 65 70 75 80  
 Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
 85 90 95  
 Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
 100 105 110  
 Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
 115 120 125  
 Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
 130 135 140  
 Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
 145 150 155 160  
 Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
 165 170 175

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Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys  
 180 185 190  
 Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg  
 195 200 205  
 Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn  
 210 215 220  
 Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile  
 225 230 235 240  
 Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala  
 245 250 255  
 Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu  
 260 265 270  
 Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu  
 275 280 285  
 Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp  
 290 295 300  
 Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu  
 305 310 315 320  
 Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp  
 325 330 335  
 Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala  
 340 345 350  
 Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys  
 355 360 365  
 Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln  
 370 375 380  
 Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile  
 385 390 395 400  
 Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser  
 405 410 415  
 Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val  
 420 425 430  
 Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn  
 435 440 445  
 Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser  
 450 455 460  
 Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys  
 465 470 475 480  
 Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu  
 485 490 495  
 Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn  
 500 505 510  
 Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser  
 515 520 525  
 Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg

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530					535					540					
Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr
545					550					555					560
Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met
				565					570					575	
Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His
			580					585					590		
Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly
		595					600					605			
Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	
	610					615					620				
Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile
	625					630					635				640
Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val
				645					650					655	
Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu
			660					665						670	
Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile
		675					680					685			
Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr
	690					695					700				
Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu
	705					710					715				720
Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala
				725					730					735	
Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp
			740					745					750		
Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val
		755					760					765			
Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg
						775					780				
Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser
	785					790					795				800
His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr
				805					810					815	
Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu
			820					825					830		
Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly
				835			840					845			
Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala
	850					855					860				
Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg
	865					870					875				880
Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys

CAAGCCGGGC	GTTCGGAGCT	GTGCCC GGCC	CCGCTT CAGC	ACCGCGGACA	GCGCCGGCCG		60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC		120
CCGGGACC GC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGGCCG	GGCGAGCGCA		180
GGACGGCCCCG	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTT CGCG	CCGCGCAGAG		240
CCAGGCCCGC	GGCCCGAGCC	C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala 1 5 10					291
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 15 20 25							339
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 30 35 40							387
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 45 50 55							435
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 60 65 70							483
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 75 80 85 90							531
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 95 100 105							579

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GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
235					240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
				255				260						265		
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
			270					275					280			
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
		285				290						295				
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTG	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
	300					305					310					
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
315					320					325					330	
GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	1299
Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	
				335				340						345		
ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	1347
Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	
			350					355					360			
GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	1395
Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	



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365					370					375							
AAC Asn	CGC Arg	AAG Lys	CTG Leu	GTG Val	CAA Gln	GTG Val	GGC Gly	ATC Ile	TAC Tyr	AAT Asn	GGC Gly	ACC Thr	CAC His	GTC Val	ATC Ile	1443	
380					385					390							
CCT Pro	AAT Asn	GAC Asp	AGG Arg	AAG Lys	ATC Ile	ATC Ile	TGG Trp	CCA Pro	GGC Gly	GGA Gly	GAG Glu	ACA Thr	GAG Glu	AAG Lys	CCT Pro	1491	
395					400					405					410		
CGA Arg	GGG Gly	TAC Tyr	CAG Gln	ATG Met	TCC Ser	ACC Thr	AGA Arg	CTG Leu	AAG Lys	ATT Ile	GTG Val	ACG Thr	ATC Ile	CAC His	CAG Gln	1539	
415					420					425					430		
GAG Glu	CCC Pro	TTC Phe	GTG Val	TAC Tyr	GTC Val	AAG Lys	CCC Pro	ACG Thr	CTG Leu	AGT Ser	GAT Asp	GGG Gly	ACA Thr	TGC Cys	AAG Lys	1587	
430					435					440					445		
GAG Glu	GAG Glu	TTC Phe	ACA Thr	GTC Val	AAC Asn	GGC Gly	GAC Asp	CCA Pro	GTC Val	AAG Lys	AAG Lys	GTG Val	ATC Ile	TGC Cys	ACC Thr	1635	
445					450					455					460		
GGG Gly	CCC Pro	AAC Asn	GAC Asp	ACG Thr	TCG Ser	CCG Pro	GGC Gly	AGC Ser	CCC Pro	CGC Arg	CAC His	ACG Thr	GTG Val	CCT Pro	CAG Gln	1683	
460					465					470					475		
TGT Cys	TGC Cys	TAC Tyr	GGC Gly	TTT Phe	TGC Cys	ATC Ile	GAC Asp	CTG Leu	CTC Leu	ATC Ile	AAG Lys	CTG Leu	GCA Ala	CGG Arg	ACC Thr	1731	
475					480					485					490		
ATG Met	AAC Asn	TTC Phe	ACC Thr	TAC Tyr	GAG Glu	GTG Val	CAC His	CTG Leu	GTG Val	GCA Ala	GAT Asp	GGC Gly	AAG Lys	TTC Phe	GGC Gly	1779	
495					500					505					510		
ACA Thr	CAG Gln	GAG Glu	CGG Arg	GTG Val	AAC Asn	AAC Asn	AGC Ser	AAC Asn	AAG Lys	AAG Lys	GAG Glu	TGG Trp	AAT Asn	GGG Gly	ATG Met	1827	
510					515					520					525		
ATG Met	GGC Gly	GAG Glu	CTG Leu	CTC Leu	AGC Ser	GGG Gly	CAG Gln	GCA Ala	GAC Asp	ATG Met	ATC Ile	GTG Val	GCG Ala	CCG Pro	CTA Leu	1875	
525					530					535					540		
ACC Thr	ATA Ile	AAC Asn	AAC Asn	GAG Glu	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro	TTC Phe	1923	
540					545					550					555		
AAG Lys	TAC Tyr	CAG Gln	GGC Gly	CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro	CGG Arg	AGC Ser	1971	
555					560					565					570		
ACG Thr	CTG Leu	GAC Asp	TCG Ser	TTC Phe	ATG Met	CAG Gln	CCG Pro	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu	TGG Trp	CTG Leu	CTG Leu	2019	
575					580					585					590		
GTG Val	GGG Gly	CTG Leu	TCG Ser	GTG Val	CAC His	GTG Val	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	2067	
590					595					600					605		
CGC Arg	TTC Phe	AGC Ser	CCC Pro	TTC Phe	GGC Gly	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	2115	
605					610					615					620		
GAG Glu	GAC Asp	GCA Ala	CTG Leu	ACC Thr	CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met	TGG Trp	TTC Phe	TCC Ser	TGG Trp	GGC Gly	GTC Val	2163	
620					625					630					635		
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211	

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Leu 635	Leu	Asn	Ser	Gly	Ile 640	Gly	Glu	Gly	Ala	Pro 645	Arg	Ser	Phe	Ser	Ala 650	
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met 655	Val	Trp	Ala	Gly	Phe 660	Ala	Met	Ile	Ile	Val 665	Ala	
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala 670	Asn	Leu	Ala	Ala	Phe 675	Leu	Val	Leu	Asp	Arg 680	Pro	Glu	
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile 685	Thr	Gly	Ile	Asn	Asp 690	Pro	Arg	Leu	Arg	Asn 695	Pro	Ser	Asp	
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe 700	Ile	Tyr	Ala	Thr	Val 705	Lys	Gln	Ser	Ser	Val 710	Asp	Ile	Tyr	Phe	
CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	2451
Arg	Arg	Gln	Val	Glu 715	Leu 720	Ser	Thr	Met	Tyr	Arg 725	His	Met	Glu	Lys	His 730	
AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	2499
Asn	Tyr	Glu	Ser	Ala 735	Ala	Glu	Ala	Ile	Gln 740	Ala	Val	Arg	Asp	Asn 745	Lys	
CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	2547
Leu	His	Ala 750	Phe	Ile	Trp	Asp	Ser	Ala 755	Val	Leu	Glu	Phe	Glu 760	Ala	Ser	
CAG	AAG	TGC	GAC	CTG	GTG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	GGC	2595
Gln	Lys	Cys 765	Asp	Leu	Val	Thr	Thr 770	Gly	Glu	Leu	Phe	Phe 775	Arg	Ser	Gly	
TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	2643
Phe	Gly 780	Ile	Gly	Met	Arg	Lys 785	Asp	Ser	Pro	Trp	Lys 790	Gln	Asn	Val	Ser	
CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	2691
Leu	Ser	Ile	Leu	Lys 800	Ser	His	Glu	Asn	Gly	Phe 805	Met	Glu	Asp	Leu	Asp 810	
AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	2739
Lys	Thr	Trp	Val	Arg 815	Tyr	Gln	Glu	Cys	Asp 820	Ser	Arg	Ser	Asn	Ala 825	Pro	
GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	2787
Ala	Thr	Leu 830	Thr	Phe	Glu	Asn	Met	Ala 835	Gly	Val	Phe	Met	Leu 840	Val	Ala	
GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	2835
Gly	Gly	Ile 845	Val	Ala	Gly	Ile	Phe 850	Leu	Ile	Phe	Ile	Glu 855	Ile	Ala	Tyr	
AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	2883
Lys	Arg 860	His	Lys	Asp	Ala	Arg 865	Arg	Lys	Gln	Met	Gln 870	Leu	Ala	Phe	Ala	
GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	2931
Ala	Val	Asn	Val	Trp 875	Arg 880	Lys	Asn	Leu	Gln	Asp 885	Arg	Lys	Ser	Gly	Arg 890	
GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	2979
Ala	Glu	Pro	Asp	Pro 895	Lys	Lys	Lys	Ala 900	Thr	Phe	Arg	Ala	Ile	Thr 905	Ser	

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ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG	3027
Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu	
910 915 920	
GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC	3075
Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser	
925 930 935	
GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC	3123
Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala	
940 945 950	
ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC	3171
Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro	
955 960 965 970	
GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC	3219
Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His	
975 980 985	
CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA	3272
Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	
990 995	
CG	3274

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 997 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	

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Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala	
				165					170					175		
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys	
			180					185					190			
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg	
		195					200					205				
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	
	210					215					220					
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	
225					230					235					240	
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	
				245					250					255		
Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	
		260						265					270			
Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	
		275					280					285				
Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	
	290					295					300					
Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	Glu	Leu	Leu	Glu	Lys	Glu	
305					310					315					320	
Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	
			325					330						335		
Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	
		340						345					350			
Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	
		355					360					365				
Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	
	370					375					380					
Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	
385					390					395					400	
Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	
			405						410					415		
Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	
		420						425					430			
Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	
		435					440					445				
Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	
	450					455					460					
Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	
465					470					475					480	
Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	
			485						490						495	
Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	
		500						505					510			
Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	

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515	520	525
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg		
530	535	540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr		
545	550	555
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met		
	565	570
		575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His		
	580	585
		590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly		
	595	600
		605
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu		
	610	615
		620
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile		
	625	630
		635
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val		
	645	650
		655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu		
	660	665
		670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile		
	675	680
		685
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr		
	690	695
		700
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu		
	705	710
		715
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala		
	725	730
		735
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp		
	740	745
		750
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val		
	755	760
		765
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg		
	770	775
		780
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser		
	785	790
		795
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr		
	805	810
		815
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu		
	820	825
		830
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly		
	835	840
		845
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala		
	850	855
		860
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		

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865		870		875		880
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys	885		890		895	
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe	900		905		910	
Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln	915		920		925	
Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro	930		935		940	
Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser	945		950		955	960
Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu		965		970		975
Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser		980		985		990
Arg Cys Met Gln Trp	995					

## (2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3070 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3051

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC GCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCCG GGGCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	10
1 5	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	25
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	40
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435

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Arg	Glu	Ala	Val	Asn	Gln	Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	
		45					50					55				
CAG	CTC	AAT	GCC	ACC	TCC	GTC	ACG	CAC	AAG	CCC	AAC	GCC	ATC	CAG	ATG	483
Gln	Leu	Asn	Ala	Thr	Ser	Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	
	60					65					70					
GCT	CTG	TCG	GTG	TGC	GAG	GAC	CTC	ATC	TCC	AGC	CAG	GTC	TAC	GCC	ATC	531
Ala	Leu	Ser	Val	Cys	Glu	Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	
	75				80					85					90	
CTA	GTT	AGC	CAT	CCA	CCT	ACC	CCC	AAC	GAC	CAC	TTC	ACT	CCC	ACC	CCT	579
Leu	Val	Ser	His	Pro	Pro	Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	
				95					100					105		
GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
			110					115					120			
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
		125					130					135				
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
	140					145					150					
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
	155				160					165					170	
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175					180					185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
			190					195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
		205					210					215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
	220					225					230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
	235				240					245					250	
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255					260					265		
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
			270					275					280			
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
		285					290					295				
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
	300					305					310					

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GTG Val 315	CAA Gln Val	GTG Val	GGC Gly	ATC Ile	TAC Tyr 320	AAT Asn	GGC Gly	ACC Thr	CAC His	GTC Val 325	ATC Ile	CCT Pro	AAT Asn	GAC Asp	AGG Arg 330	1251
AAG Lys	ATC Ile	ATC Ile	TGG Trp 335	CCA Pro	GGC Gly	GGA Gly	GAG Glu	ACA Thr	GAG Glu 340	AAG Lys	CCT Pro	CGA Arg	GGG Gly	TAC Tyr 345	CAG Gln	1299
ATG Met	TCC Ser	ACC Thr	AGA Arg 350	CTG Leu	AAG Lys	ATT Ile	GTG Val 355	ACG Thr	ATC Ile	CAC His	CAG Gln	GAG Glu 360	CCC Pro	TTC Phe	GTG Val	1347
TAC Tyr	GTC Val	AAG Lys 365	CCC Pro	ACG Thr	CTG Leu	AGT Ser	GAT Asp 370	GGG Gly	ACA Thr	TGC Cys	AAG Lys	GAG Glu 375	GAG Glu	TTC Phe	ACA Thr	1395
GTC Val 380	AAC Asn	GGC Gly	GAC Asp	CCA Pro	GTC Val 385	AAG Lys	AAG Lys	GTG Val	ATC Ile	TGC Cys	ACC Thr 390	GGG Gly	CCC Pro	AAC Asn	GAC Asp	1443
ACG Thr 395	TCG Ser	CCG Pro	GGC Gly	AGC Ser	CCC Pro 400	CGC Arg	CAC His	ACG Thr	GTG Val 405	CCT Pro	CAG Gln	TGT Cys	TGC Cys	TAC Tyr	GGC Gly 410	1491
TTT Phe	TGC Cys	ATC Ile	GAC Asp	CTG Leu 415	CTC Leu	ATC Ile	AAG Lys	CTG Leu 420	GCA Ala	CGG Arg	ACC Thr	ATG Met	AAC Asn	TTC Phe 425	ACC Thr	1539
TAC Tyr	GAG Glu	GTG Val	CAC His 430	CTG Leu	GTG Val	GCA Ala	GAT Asp	GGC Gly 435	AAG Lys	TTC Phe	GGC Gly	ACA Thr	CAG Gln 440	GAG Glu	CGG Arg	1587
GTG Val	AAC Asn	AAC Asn 445	AGC Ser	AAC Asn	AAG Lys	AAG Lys	GAG Glu 450	TGG Trp	AAT Asn	GGG Gly	ATG Met	ATG Met 455	GGC Gly	GAG Glu	CTG Leu	1635
CTC Leu 460	AGC Ser	GGG Gly	CAG Gln	GCA Ala	GAC Asp	ATG Met 465	ATC Ile	GTG Val	GCG Ala	CCG Pro	CTA Leu 470	ACC Thr	ATA Ile	AAC Asn	AAC Asn	1683
GAG Glu 475	CGC Arg	GCG Ala	CAG Gln	TAC Tyr	ATC Ile 480	GAG Glu	TTT Phe	TCC Ser	AAG Lys	CCC Pro 485	TTC Phe	AAG Lys	TAC Tyr	CAG Gln	GGC Gly 490	1731
CTG Leu	ACT Thr	ATT Ile	CTG Leu	GTC Val 495	AAG Lys	AAG Lys	GAG Glu	ATT Ile	CCC Pro 500	CGG Arg	AGC Ser	ACG Thr	CTG Leu	GAC Asp 505	TCG Ser	1779
TTC Phe	ATG Met	CAG Gln 510	CCG Pro	TTC Phe	CAG Gln	AGC Ser	ACA Thr	CTG Leu 515	TGG Trp	CTG Leu	CTG Leu	GTG Val	GGG Gly 520	CTG Leu	TCG Ser	1827
GTG Val	CAC His	GTG Val 525	GTG Val	GCC Ala	GTG Val	ATG Met	CTG Leu 530	TAC Tyr	CTG Leu	CTG Leu	GAC Asp	CGC Arg 535	TTC Phe	AGC Ser	CCC Pro	1875
TTC Phe 540	GGC Gly	CGG Arg	TTC Phe	AAG Lys	GTG Val	AAC Asn 545	AGC Ser	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAG Glu	GAC Asp	GCA Ala	CTG Leu	1923
ACC Thr 555	CTG Leu	TCC Ser	TCG Ser	GCC Ala	ATG Met 560	TGG Trp	TTC Phe	TCC Ser	TGG Trp	GGC Gly 565	GTC Val	CTG Leu	CTC Leu	AAC Asn	TCC Ser 570	1971
GGC Gly	ATC Ile	GGG Gly	GAA Glu	GGC Gly 575	GCC Ala	CCC Pro	AGA Arg	AGC Ser	TTC Phe 580	TCA Ser	GCG Ala	CGC Arg	ATC Ile	CTG Leu 585	GGC Gly	2019



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ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC	2067
Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala	
590 595 600	
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG	2115
Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr	
605 610 615	
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC	2163
Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr	
620 625 630	
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG	2211
Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val	
635 640 650	
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT	2259
Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser	
655 660 665	
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC	2307
Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe	
670 675 680	
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC	2355
Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp	
685 690 695	
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC	2403
Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly	
700 705 710	
ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC	2451
Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu	
715 720 725 730	
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT	2499
Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val	
735 740 745	
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT	2547
Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr	
750 755 760	
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG	2595
Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val	
765 770 775	
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG	2643
Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys	
780 785 790	
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG	2691
Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val	
795 800 805 810	
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC	2739
Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp	
815 820 825	
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC	2787
Pro Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser	
830 835 840	
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT	2835
Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys	
845 850 855	

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CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG	2883
Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro	
860 865 870	
CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA	2931
Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg	
875 880 885 890	
ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC	2979
Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg	
895 900 905	
GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC	3027
Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro	
910 915 920	
ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG	3070
Thr Ser Arg Cys Met Gln Trp	
925 930	

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 929 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys	
180 185 190	

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Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg  
 195 200 205  
 Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn  
 210 215 220  
 Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile  
 225 230 235 240  
 Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala  
 245 250 255  
 Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro  
 260 265 270  
 Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr  
 275 280 285  
 Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr  
 290 295 300  
 Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr  
 305 310 315 320  
 Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly  
 325 330 335  
 Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys  
 340 345 350  
 Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu  
 355 360 365  
 Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val  
 370 375 380  
 Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro  
 385 390 395 400  
 Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu  
 405 410 415  
 Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val  
 420 425 430  
 Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys  
 435 440 445  
 Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp  
 450 455 460  
 Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile  
 465 470 475 480  
 Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys  
 485 490 495  
 Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln  
 500 505 510  
 Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val  
 515 520 525  
 Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val  
 530 535 540  
 Asn Ser Glu Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met

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545					550						555				560
Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala
				565					570					575	
Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe
			580					585					590		
Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu
		595					600					605			
Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg
	610					615					620				
Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser
625					630					635					640
Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr
				645					650					655	
Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln
			660					665						670	
Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val
		675					680					685			
Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu
	690					695					700				
Leu	Phe	Phe	Arg	Ser	Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro
705					710					715					720
Trp	Lys	Gln	Asn	Val	Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly
				725					730					735	
Phe	Met	Glu	Asp	Leu	Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp
			740					745					750		
Ser	Arg	Ser	Asn	Ala	Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly
			755				760					765			
Val	Phe	Met	Leu	Val	Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile
	770					775					780				
Phe	Ile	Glu	Ile	Ala	Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln
785					790					795					800
Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln
				805					810					815	
Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr
			820					825					830		
Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg
		835					840					845			
Ser	Ser	Lys	Asp	Thr	Leu	Ala	Arg	Asp	Cys	Leu	Gln	Pro	Cys	Pro	Ala
	850					855					860				
Pro	Trp	Ala	Arg	Glu	Ser	Ala	Thr	Arg	Pro	Pro	Pro	Pro	Ser	Leu	Arg
865					870					875					880
Val	Arg	Asp	Arg	Pro	Ala	Thr	Leu	Tyr	Arg	Thr	Ser	Thr	Pro	Arg	Ala
				885					890					895	
Arg	Ala	Arg	Ala	Phe	Pro	Val	Arg	Ser	Arg	Ala	Leu	Pro	Leu	Arg	Pro

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900 905 910

Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln

915 920 925

Trp

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2326 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..2324

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CC GGC CAC GTG TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT	47
Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp	
1 5 10 15	
GCG CCC CCC GCC ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG	95
Ala Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu	
20 25 30	
AGC TGG CGC CTC AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT	143
Ser Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile	
35 40 45	
CTG GCC CTG GGC GCC CAC AGC TAC TGG CGC CAG CAT GGA ACC CTG CCA	191
Leu Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro	
50 55 60	
GCC CCG GCC GGG GAC TGC CGT GTT CAC CCT GGG CCC GTC AGC CCT GCC	239
Ala Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala	
65 70 75	
CGG GAG GCC TTC TAC AGG CAC CTA CTG AAT GTC ACC TGG GAG GGC CGA	287
Arg Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg	
80 85 90 95	
GAC TTC TCC TTC AGC CCT GGT GGG TAC CTG GTC CAG CCC ACC ATG GTG	335
Asp Phe Ser Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val	
100 105 110	
GTG ATC GCC CTC AAC CGG CAC CGC CTC TGG GAG ATG GTG GGG CGC TGG	383
Val Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp	
115 120 125	
GAG CAT GGC GTC CTA TAC ATG AAG TAC CCC GTG TGG CCT CGC TAC AGT	431
Glu His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser	
130 135 140	
GCC TCT CTG CAG CCT GTG GTG GAC AGT CGG CAC CTG ACG GTG GCC ACG	479
Ala Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr	
145 150 155	

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CTG Leu 160	GAA Glu	GAG Glu	CGG Arg	CCC Pro	TTT Phe 165	GTC Val	ATC Ile	GTG Val	GAG Glu	AGC Ser 170	CCT Pro	GAC Asp	CCT Pro	GGC Gly	ACA Thr 175	527
GGA Gly	GGC Gly	TGT Cys	GTC Val	CCC Pro 180	AAC Asn	ACC Thr	GTG Val	CCC Pro	TGC Cys 185	CGC Arg	AGG Arg	CAG Gln	AGC Ser	AAC Asn 190	CAC His	575
ACC Thr	TTC Phe	AGC Ser 195	AGC Ser 195	GGG Gly	GAC Asp	GTG Val	GCC Ala	CCC Pro 200	TAC Tyr	ACC Thr	AAG Lys	CTC Leu	TGC Cys 205	TGT Cys	AAG Lys	623
GGA Gly	TTC Phe	TGC Cys 210	ATC Ile	GAC Asp	ATC Ile	CTC Leu	AAG Lys 215	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val 220	GTC Val	AAA Lys	TTC Phe	671
TCC Ser	TAC Tyr 225	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val 230	ACC Thr	AAC Asn	GGC Gly	AAG Lys 235	CAT His	GGC Gly	AAG Lys	CGG Arg	GTG Val	719
CGC Arg 240	GGC Gly	GTA Val	TGG Trp	AAC Asn	GGC Gly 245	ATG Met	ATT Ile	GGG Gly	GAG Glu	GTG Val 250	TAC Tyr	TAC Tyr	AAG Lys	CGG Arg	GCA Ala 255	767
GAC Asp	ATG Met	GCC Ala	ATC Ile	GGC Gly 260	TCC Ser	CTC Leu	ACC Thr	ATC Ile	AAT Asn 265	GAG Glu	GAA Glu	CGC Arg	TCC Ser	GAG Glu 270	ATC Ile	815
GTA Val	GAC Asp	TTC Phe	TCT Ser 275	GTA Val	CCC Pro	TTT Phe	GTG Val	GAG Glu 280	ACG Thr	GGC Gly	ATC Ile	AGT Ser	GTG Val 285	ATG Met	GTG Val	863
GCT Ala	CGC Arg	AGC Ser 290	AAT Asn	GGC Gly	ACC Thr	GTC Val	TCC Ser 295	CCC Pro	TCG Ser	GCC Ala	TTC Phe	TTG Leu 300	GAG Glu	CCA Pro	TAT Tyr	911
AGC Ser 305	CCT Pro	GCA Ala	GTG Val	TGG Trp	GTG Val	ATG Met 310	ATG Met	TTT Phe	GTC Val	ATG Met	TGC Cys 315	CTC Leu	ACT Thr	GTG Val	GTG Val	959
GCC Ala 320	ATC Ile	ACC Thr	GTC Val	TTC Phe	ATG Met 325	TTC Phe	GAG Glu	TAC Tyr	TTC Phe	AGC Ser 330	CCT Pro	GTC Val	AGC Ser	TAC Tyr	AAC Asn 335	1007
CAG Gln	AAC Asn	CTC Leu	ACC Thr	AGA Arg 340	GGC Gly	AAG Lys	AAG Lys	TCC Ser	GGG Gly 345	GGC Gly	CCA Pro	GCT Ala	TTC Phe	ACT Thr 350	ATC Ile	1055
GGC Gly	AAG Lys	TCC Ser 355	GTG Val	TGG Trp	CTG Leu	CTG Leu	TGG Trp	GCG Ala 360	CTG Leu	GTC Val	TTC Phe	AAC Asn	AAC Asn 365	TCA Ser	GTG Val	1103
CCC Pro	ATC Ile	GAG Glu 370	AAC Asn	CCG Pro	CGG Arg	GGC Gly	ACC Thr 375	ACC Thr	AGC Ser	AAG Lys	ATC Ile	ATG Met 380	GTT Val	CTG Leu	GTC Val	1151
TGG Trp 385	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val	ATC Ile 390	TTC Phe	CTC Leu	GCC Ala	AGA Arg	TAC Tyr 395	ACG Thr	GCC Ala	AAC Asn	CTG Leu	1199
GCC Ala 400	GCC Ala	TTC Phe	ATG Met	ATC Ile	CAA Gln 405	GAG Glu	CAA Gln	TAC Tyr	ATC Ile	GAC Asp 410	ACT Thr	GTG Val	TCG Ser	GGC Gly	CTC Leu 415	1247
AGT Ser	GAC Asp	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg	CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr	CCA Pro	CCT Pro	TTC Phe	CGC Arg	1295

				420				425				430				
TTC Phe	GGC Gly	ACG Thr	GTG Val 435	CCC Pro	AAC Asn	GGC Gly	AGC Ser	ACG Thr 440	GAG Glu	CGG Arg	AAC Asn	ATC Ile	CGC Arg 445	AGT Ser	AAC Asn	1343
TAC Tyr	CGT Arg	GAC Asp 450	ATG Met	CAC His	ACC Thr	CAC His	ATG Met 455	GTC Val	AAG Lys	TTC Phe	AAC Asn	CAG Gln 460	CGC Arg	TCG Ser	GTG Val	1391
GAG Glu	GAC Asp 465	GCG Ala	CTC Leu	ACC Thr	AGC Ser	CTC Leu 470	AAG Lys	ATG Met	GGC Gly	AAG Lys	GAC Asp 475	GAG Glu	GGC Gly	TGC Cys	AAG Lys	1439
CTG Leu 480	GTC Val	ACC Thr	ATT Ile	GGG Gly	TCT Ser 485	GGC Gly	AAG Lys	GTC Val	TTT Phe 490	GCT Ala	ACC Thr	ACT Thr	GGC Gly	TAC Tyr	GGC Gly 495	1487
ATC Ile	GCC Ala	ATG Met	CAG Gln	AAG Lys 500	GAC Asp	TCC Ser	CAC His	TGG Trp	AAG Lys 505	CGG Arg	GCC Ala	ATA Ile	GAC Asp	CTG Leu 510	GCG Ala	1535
CTC Leu	TTG Leu	CAG Gln	TTC Phe 515	CTG Leu	GGG Gly	GAC Asp	GGA Gly	GAG Glu 520	ACA Thr	CAG Gln	AAA Lys	CTG Leu	GAG Glu 525	ACA Thr	GTG Val	1583
TGG Trp	CTC Leu	TCA Ser 530	GGG Gly	ATC Ile	TGC Cys	CAG Gln	AAT Asn 535	GAG Glu	AAG Lys	AAC Asn	GAG Glu	GTG Val 540	ATG Met	AGC Ser	AGC Ser	1631
AAG Lys	CTG Leu 545	GAC Asp	ATC Ile	GAC Asp	AAC Asn	ATG Met 550	GGA Gly	GGC Gly	GTC Val	TTC Phe	TAC Tyr 555	ATG Met	CTG Leu	CTG Leu	GTG Val	1679
GCC Ala 560	ATG Met	GGG Gly	CTG Leu	GCC Ala	CTG Leu 565	CTG Leu	GTC Val	TTC Phe	GCC Ala	TGG Trp 570	GAG Glu	CAC His	CTG Leu	GTC Val	TAC Tyr 575	1727
TGG Trp	AAG Lys	CTG Leu	CGC Arg	CAC His 580	TCG Ser	GTG Val	CCC Pro	AAC Asn	TCA Ser 585	TCC Ser	CAG Gln	CTG Leu	GAC Asp	TTC Phe 590	CTG Leu	1775
CTG Leu	GCT Ala	TTC Phe	AGC Ser 595	AGG Arg	GGC Gly	ATC Ile	TAC Tyr	AGC Ser 600	TGC Cys	TTC Phe	AGC Ser	GGG Gly	GTG Val 605	CAG Gln	AGC Ser	1823
CTC Leu	GCC Ala	AGC Ser 610	CCA Pro	CCG Pro	CGG Arg	CAG Gln	GCC Ala 615	AGC Ser	CCG Pro	GAC Asp	CTC Leu	ACG Thr 620	GCC Ala	AGC Ser	TCG Ser	1871
GCC Ala	CAG Gln 625	GCC Ala	AGC Ser	GTG Val	CTC Leu	AAG Lys 630	ATT Ile	CTG Leu	CAG Gln	GCA Ala	GCC Ala 635	CGC Arg	GAC Asp	ATG Met	GTG Val	1919
ACC Thr 640	ACG Thr	GCG Ala	GGC Gly	GTA Val	AGC Ser 645	AAC Asn	TCC Ser	CTG Leu	GAC Asp	CGC Arg 650	GCC Ala	ACT Thr	CGC Arg	ACC Thr	ATC Ile 655	1967
GAG Glu	AAT Asn	TGG Trp	GGT Gly 660	GGC Gly	GGC Gly	CGC Arg	CGT Arg	GCG Ala	CCC Pro 665	CCA Pro	CCG Pro	TCC Ser	CCC Pro	TGC Cys 670	CCG Pro	2015
ACC Thr	CCG Pro	CGG Arg	TCT Ser 675	GGC Gly	CCC Pro	AGC Ser	CCA Pro	TGC Cys 680	CTG Leu	CCC Pro	ACC Thr	CCC Pro	GAC Asp 685	CCG Pro	CCC Pro	2063
CCA	GAG	CCG	AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	2111

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Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala		
		690					695					700					
GCG	CTT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	2159	
Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro		
	705					710					715						
GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	2207	
Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp		
	720				725					730					735		
GAG	GCG	CGG	TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	2255	
Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser		
				740					745					750			
GCC	TCC	GAG	CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	2303	
Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe		
			755					760					765				
CCT	CGA	GCC	GAC	CGA	TCC	GGC	CG									2326	
Pro	Arg	Ala	Asp	Arg	Ser	Gly											
		770															

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly	His	Val	Trp	Leu	Val	Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala		
1				5					10					15			
Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser		
			20					25					30				
Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu		
		35				40						45					
Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala		
	50				55						60						
Pro	Ala	Gly	Asp	Cys	Arg	Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg		
	65			70						75					80		
Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp		
				85				90						95			
Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val		
			100					105					110				
Ile	Ala	Leu	Asn	Arg	His	Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu		
	115						120					125					
His	Gly	Val	Leu	Tyr	Met	Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala		
	130					135					140						
Ser	Leu	Gln	Pro	Val	Val	Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu		
	145				150					155					160		
Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly		
				165					170					175			



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Gly	Cys	Val	Pro	Asn	Thr	Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr
			180					185					190		
Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly
		195					200					205			
Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser
	210					215					220				
Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg
225					230					235					240
Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp
				245					250					255	
Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val
			260					265					270		
Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala
		275					280					285			
Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser
	290					295					300				
Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala
305					310					315					320
Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln
				325					330					335	
Asn	Leu	Thr	Arg	Gly	Lys	Lys	Ser	Gly	Gly	Pro	Ala	Phe	Thr	Ile	Gly
			340					345					350		
Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro
		355					360					365			
Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Leu	Val	Trp
	370					375					380				
Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala
385					390					395					400
Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser
				405					410					415	
Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe
			420					425					430		
Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr
		435					440					445			
Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu
	450					455					460				
Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu
465					470					475					480
Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile
				485					490					495	
Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu
			500					505					510		
Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp
		515					520					525			

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Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys  
 530 535 540  
 Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala  
 545 550 555 560  
 Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp  
 565 570 575  
 Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu  
 580 585 590  
 Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu  
 595 600 605  
 Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala  
 610 615 620  
 Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr  
 625 630 635 640  
 Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu  
 645 650 655  
 Asn Trp Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr  
 660 665 670  
 Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro  
 675 680 685  
 Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala  
 690 695 700  
 Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly  
 705 710 715 720  
 Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu  
 725 730 735  
 Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala  
 740 745 750  
 Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro  
 755 760 765  
 Arg Ala Asp Arg Ser Gly  
 770

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3698 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 3...3698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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TG	GAG	ATC	CAG	CCG	CTC	ACA	GTT	GGG	GTC	AAC	ACC	ACC	AAC	CCC	AGC	47
Glu	Ile	Gln	Pro	Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser		
1					5				10					15		
AGC	CTC	CTC	ACC	CAG	ATC	TGC	GGC	CTC	CTG	GGT	GCT	GCC	CAC	GTC	CAC	95
Ser	Leu	Leu	Thr	Gln	Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	
				20					25					30		
GGC	ATT	GTC	TTT	GAG	GAC	AAC	GTG	GAC	ACC	GAG	GCG	GTG	GCC	CAG	ATC	143
Gly	Ile	Val	Phe	Glu	Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	
			35				40						45			
CTT	GAC	TTC	ATC	TCC	TCC	CAG	ACC	CAT	GTG	CCC	ATC	CTC	AGC	ATC	AGC	191
Leu	Asp	Phe	Ile	Ser	Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	
			50				55					60				
GGA	GGC	TCT	GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	239
Gly	Gly	Ser	Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	
	65					70					75					
CTG	CAG	CTG	GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	287
Leu	Gln	Leu	Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	
80					85					90					95	
GTG	CTG	GAA	GAG	TAC	GAC	TGG	AGC	GCC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	335
Val	Leu	Glu	Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	
				100					105					110		
CAC	CCG	GGC	CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	CGC	GCC	GTC	GCC	GAC	383
His	Pro	Gly	His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	
			115					120					125			
GCC	AGC	CAC	GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	431
Ala	Ser	His	Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	
			130				135					140				
GAC	CCG	GGA	GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	479
Asp	Pro	Gly	Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	
	145					150					155					
GAC	GCG	CCC	GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	527
Asp	Ala	Pro	Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	
160					165					170					175	
CTC	TTC	GCC	GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	575
Leu	Phe	Ala	Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	
				180					185					190		
TGG	CTG	GTG	CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	623
Trp	Leu	Val	Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	
			195					200					205			
ACC	TTC	CCC	GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	671
Thr	Phe	Pro	Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	
			210				215					220				
AGC	CTG	CGC	CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	719
Ser	Leu	Arg	Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	
	225					230					235					
GCC	CAC	AGC	TAC	TGG	CGC	CAG	CAT	GGA	ACC	CAG	AAG	GGG	GTG	TGC	CAG	767
Ala	His	Ser	Tyr	Trp	Arg	Gln	His	Gly	Thr	Gln	Lys	Gly	Val	Cys	Gln	
240					245					250					255	
CCC	CGG	CCG	GGG	ACT	GCC	GTG	TTC	ACC	CTG	GGC	CCG	TCA	GCC	CTG	CCC	815
Pro	Arg	Pro	Gly	Thr	Ala	Val	Phe	Thr	Leu	Gly	Pro	Ser	Ala	Leu	Pro	
				260					265					270		

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GGG Gly	AGG Arg	CCT Pro	TCT Ser	ACA Thr	GGC Gly	ACC Thr	TAC Tyr	TGA *	ATG Met	TCA Ser	CCT Pro	GGG Gly	AGG Arg	GCC Ala	GAG Glu	863
			275					280					285			
ACT Thr	TCT Ser	CCT Pro	TCA Ser	GCC Ala	CTG Leu	GTG Val	GGT Gly	ACC Thr	TGG Trp	TCC Ser	AGC Ser	CCA Pro	CCA Pro	TGG Trp	TGG Trp	911
		290					295					300				
TGA *	TCG Ser	CCC Pro	TCA Ser	ACC Thr	GGC Gly	ACC Thr	GCC Ala	TCT Ser	GGG Gly	AGA Arg	TGG Trp	TGG Trp	GGC Gly	GCT Ala	GGG Gly	959
	305					310					315					
AGC Ser	ATG Met	GCG Ala	TCC Ser	TAT Tyr	ACA Thr	TGA *	AGT Ser	ACC Thr	CCG Pro	TGT Cys	GGC Gly	CTC Leu	GCT Ala	ACA Thr	GTG Val	1007
320					325					330					335	
CCT Pro	CTC Leu	TGC Cys	AGC Ser	CTG Leu	TGG Trp	TGG Trp	ACA Thr	GTC Val	GGC Gly	ACC Thr	TGA *	CGG Arg	TGG Trp	CCA Pro	CGC Arg	1055
				340					345					350		
TGG Trp	AAG Lys	AGC Ser	GGC Gly	CCT Pro	TTG Leu	TCA Ser	TCG Ser	TGG Trp	AGA Arg	GCC Ala	CTG Leu	ACC Thr	CTG Leu	GCA Ala	CAG Gln	1103
			355					360				365				
GAG Glu	GCT Ala	GTG Val	TCC Ser	CCA Pro	ACA Thr	CCG Pro	TGC Cys	CCT Pro	GCC Ala	GCA Ala	GGC Gly	AGA Arg	GCA Ala	ACC Thr	ACA Thr	1151
		370					375					380				
CCT Pro	TCA Ser	GCA Ala	GCG Ala	GGG Gly	ACG Thr	TGG Trp	CCC Pro	CCT Pro	ACA Thr	CCA Pro	AGC Ser	TCT Ser	GCT Ala	GTA Val	AGG Arg	1199
	385					390					395					
GAT Asp	TCT Ser	GCA Ala	TCG Ser	ACA Thr	TCC Ser	TCA Ser	AGA Arg	AGC Ser	TGG Trp	CCA Pro	GAG Glu	TGG Trp	TCA Ser	AAT Asn	TCT Ser	1247
400					405					410					415	
CCT Pro	ACG Thr	ACC Thr	TGT Cys	ACC Thr	TGG Trp	TGA *	CCA Pro	ACG Thr	GCA Ala	AGC Ser	ATG Met	GCA Ala	AGC Ser	GGG Gly	TGC Cys	1295
				420					425					430		
GCG Ala	GCG Ala	TAT Tyr	GGA Gly	ACG Thr	GCA Ala	TGA *	TTG Leu	GGG Gly	AGG Arg	TGT Cys	ACT Thr	ACA Thr	AGC Ser	GGG Gly	CAG Gln	1343
			435					440					445			
ACA Thr	TGG Trp	CCA Pro	TCG Ser	GCT Ala	CCC Pro	TCA Ser	CCA Pro	TCA Ser	ATG Met	AGG Arg	AAC Asn	GCT Ala	CCG Pro	AGA Arg	TCG Ser	1391
		450					455					460				
TAG *	ACT Thr	TCT Ser	CTG Leu	TAC Tyr	CCT Pro	TTG Leu	TGG Trp	AGA Arg	CGG Arg	GCA Ala	TCA Ser	GTG Val	TGA *	TGG Trp	TGG Trp	1439
	465					470					475					
CTC Leu	GCA Ala	GCA Ala	ATG Met	GCA Ala	CCG Pro	TCT Ser	CCC Pro	CCT Pro	CGG Arg	CCT Pro	TCT Ser	TGG Trp	AGC Ser	CAT His	ATA Ile	1487
480					485					490					495	
GCC Ala	CTG Leu	CAG Gln	TGT Cys	GGG Gly	TGA *	TGA *	TGT Cys	TTG Leu	TCA Ser	TGT Cys	GCC Ala	TCA Ser	CTG Leu	TGG Trp	TGG Trp	1535
				500				505					510			
CCA Pro	TCA Ser	CCG Pro	TCT Ser	TCA Ser	TGT Cys	TCG Ser	AGT Ser	ACT Thr	TCA Ser	GCC Ala	CTG Leu	TCA Ser	GCT Ala	ACA Thr	ACC Thr	1583
			515					520					525			
AGA Arg	ACC Thr	TCA Ser	CCA Pro	GAG Glu	GCA Ala	AGA Arg	CTT Leu	TCA Ser	CTA Leu	TCG Ser	GCA Ala	AGT Ser	CCG Pro	TGT Cys	GGC Gly	1631
		530					535					540				

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TGC Cys 545	TGT Cys	GGG Gly	CGC Arg	TGG Trp	TCT Ser	TCA Ser 550	ACA Thr	ACT Thr	CAG Gln	TGC Cys	CCA Pro 555	TCG Ser	AGA Arg	ACC Thr	CGC Arg	1679
GGG Gly 560	GCA Ala	CCA Pro	CCA Pro	GCA Ala	AGA Arg 565	TCA Ser	TGG Trp	TTC Phe	TGG Trp	TCT Ser 570	GGG Gly	CCT Pro	TCT Ser	TTG Leu	CTG Leu 575	1727
TCA Ser	TCT Ser	TCC Ser	TCG Ser	CCA Pro 580	GAT Asp	ACA Thr	CGG Arg	CCA Pro	ACC Thr 585	TGG Trp	CCG Pro	CCT Pro	TCA Ser	TGA * 590	TCC Ser	1775
AAG Lys	AGC Ser	AAT Asn 595	ACA Thr	TCG Ser	ACA Thr	CTG Leu	TGT Cys	CGG Arg 600	GCC Ala	TCA Ser	GTG Val	ACA Thr	AGA Arg 605	AGT Ser	TTC Phe	1823
AGC Ser	GGC Gly	CTC Leu 610	AAG Lys	ATC Ile	AGT Ser	ACC Thr	CAC His 615	CTT Leu	TCC Ser	GCT Ala	TCG Ser	GCA Ala 620	CGG Arg	TGC Cys	CCA Pro	1871
ACG Thr 625	GCA Ala	GCA Ala	CGG Arg	AGC Ser	GGA Gly	ACA Thr 630	TCC Ser	GCA Ala	GTA Val	ACT Thr	ACC Thr 635	GTG Val	ACA Thr	TGC Cys	ACA Thr	1919
CCC Pro 640	ACA Thr	TGG Trp	TCA Ser	AGT Ser	TCA Ser 645	ACC Thr	AGC Ser	GCT Ala	CGG Arg	TGG Trp 650	AGG Arg	ACG Thr	CGC Arg	TCA Ser	CCA Pro 655	1967
GCC Ala	TCA Ser	AGA Arg	TGG Trp	GGA Gly 660	AGC Ser	TGG Trp	ATG Met	CCT Pro	TCA Ser 665	TCT Ser	ATG Met	ATG Met	CTG Leu 670	CTG Leu	TCC Ser	2015
TCA Ser	ACT Thr	ACA Thr	TGG Trp 675	CAG Gln	GCA Ala	AGG Arg	ACG Thr	AGG Arg	GCT Ala	GCA Ala	AGC Ser	TGG Trp	TCA Ser 685	CCA Pro	TTG Leu	2063
GGT Gly	CTG Leu	GCA Ala 690	AGG Arg	TCT Ser	TTG Leu	CTA Leu	CCA Pro 695	CTG Leu	GCT Ala	ACG Thr	GCA Ala	TCG Ser 700	CCA Pro	TGC Cys	AGA Arg	2111
AGG Arg 705	ACT Thr	CCC Pro	ACT Thr	GGA Gly	AGC Ser	GGG Gly 710	CCA Pro	TAG *	ACC Thr	TGG Trp	CGC Arg 715	TCT Ser	TGC Cys	AGT Ser	TCC Ser	2159
TGG Trp 720	GGG Gly	ACG Thr	GAG Glu	AGA Arg	CAC His 725	AGA Arg	AAC Asn	TGG Trp	AGA Arg	CAG Gln 730	TGT Cys	GGC Gly	TCT Ser	CAG Gln	GGA Gly 735	2207
TCT Ser	GCC Ala	AGA Arg	ATG Met	AGA Arg 740	AGA Arg	ACG Thr	AGG Arg	TGA *	TGA *	GCA Ala 745	GCA Ala	AGC Ser	TGG Trp	ACA Thr 750	TCG Ser	2255
ACA Thr	ACA Thr	TGG Trp	GAG Glu 755	CGC Ala	TCT Ser	TCT Ser	ACA Thr	TGC Cys 760	TGC Cys	TGG Trp	TGG Trp	CCA Pro	TGG Trp 765	GGC Gly	TGG Trp	2303
CCC Pro	TGC Cys	TGG Trp 770	TCT Ser	TCG Ser	CCT Pro	GGG Gly 775	AGC Ser	ACC Thr	TGG Trp	TCT Ser	ACT Thr	GGA Gly 780	AGC Ser	TGC Cys	GCC Ala	2351
ACT Thr 785	CGG Arg	TGC Cys	CCA Pro	ACT Thr	CAT His	CCC Pro 790	AGC Ser	TGG Trp	ACT Thr	TCC Ser	TGC Cys 795	TGG Trp	CTT Leu	TCA Ser	GCA Ala	2399
GGG Gly 800	GCA Ala	TCT Ser	ACA Thr	GCT Ala	GCT Ala 805	TCA Ser	GCG Ala	GGG Gly	TGC Cys	AGA Arg 810	GCC Ala	TCG Ser	CCA Pro	GCC Ala	CAC His 815	2447

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CGC	GGC	AGG	CCA	GCC	CGG	ACC	TCA	CGG	CCA	GCT	CGG	CCC	AGG	CCA	GCG	2495
Arg	Gly	Arg	Pro	Ala	Arg	Thr	Ser	Arg	Pro	Ala	Arg	Pro	Arg	Pro	Ala	
				820					825					830		
TGC	TCA	AGA	TTC	TGC	AGG	CAG	CCC	GCG	ACA	TGG	TGA	CCA	CGG	CGG	GCG	2543
Cys	Ser	Arg	Phe	Cys	Arg	Gln	Pro	Ala	Thr	Trp	*	Pro	Arg	Arg	Ala	
			835					840					845			
TAA	GCA	ACT	CCC	TGG	ACC	GCG	CCA	CTC	GCA	CCA	TCG	AGA	ATT	GGG	GTG	2591
*	Ala	Thr	Pro	Trp	Thr	Ala	Pro	Leu	Ala	Pro	Ser	Arg	Ile	Gly	Val	
		850					855					860				
GCG	GCC	GCC	GTG	CGC	CCC	CAC	CGT	CCC	CCT	GCC	CGA	CCC	CGC	GGT	CTG	2639
Ala	Ala	Ala	Val	Arg	Pro	His	Arg	Pro	Pro	Ala	Arg	Pro	Arg	Gly	Leu	
	865					870					875					
GCC	CCA	GCC	CAT	GCC	TGC	CCA	CCC	CCG	ACC	CGC	CCC	CAG	AGC	CGA	GCC	2687
Ala	Pro	Ala	His	Ala	Cys	Pro	Pro	Pro	Thr	Arg	Pro	Gln	Ser	Arg	Ala	
880					885					890					895	
CCA	CGG	GCT	GGG	GAC	CGC	CAG	ACG	GGG	GTC	GCG	CGG	CGC	TTG	TGC	GCA	2735
Pro	Arg	Ala	Gly	Asp	Arg	Gln	Thr	Gly	Val	Ala	Arg	Arg	Leu	Cys	Ala	
				900				905						910		
GGG	CTC	CGC	AGC	CCC	CGG	GCC	GCC	CCC	CGA	CGC	CGG	GGC	CGC	CCC	TGT	2783
Gly	Leu	Arg	Ser	Pro	Arg	Ala	Ala	Pro	Arg	Arg	Arg	Gly	Arg	Pro	Cys	
			915					920					925			
CCG	ACG	TCT	CCC	GAG	TGT	CGC	GCC	GCC	CAG	CCT	GGG	AGG	CGC	GGT	GGC	2831
Pro	Thr	Ser	Pro	Glu	Cys	Arg	Ala	Ala	Gln	Pro	Gly	Arg	Arg	Gly	Gly	
		930					935					940				
CGG	TGC	GGA	CCG	GGC	ACT	GCG	GGA	GGC	ACC	TCT	CGG	CCT	CCG	AGC	GGC	2879
Arg	Cys	Gly	Pro	Gly	Thr	Ala	Gly	Gly	Thr	Ser	Arg	Pro	Pro	Ser	Gly	
	945					950					955					
CCC	TGT	CGC	CCG	CGC	GCT	GTC	ACT	ACA	GCT	CCT	TTC	CTC	GAG	CCG	ACC	2927
Pro	Cys	Arg	Pro	Arg	Ala	Val	Thr	Thr	Ala	Pro	Phe	Leu	Glu	Pro	Thr	
960					965					970					975	
GAT	CCG	GCC	GCC	CCT	TCC	TCC	CGC	TCT	TCC	CGG	AGC	CCC	CGG	AGC	TGG	2975
Asp	Pro	Ala	Ala	Pro	Ser	Ser	Arg	Ser	Ser	Arg	Ser	Pro	Arg	Ser	Trp	
				980				985						990		
AGG	ACC	TGC	CGC	TGC	TCG	GTC	CGG	AGC	AGC	TGG	CCC	GGC	GGG	AGG	CCC	3023
Arg	Thr	Cys	Arg	Cys	Ser	Val	Arg	Ser	Ser	Trp	Pro	Gly	Gly	Arg	Pro	
		995					1000					1005				
TGC	TGA	ACG	CGG	CCT	GGG	CCC	GGG	GCT	CGC	GCC	CGA	GTC	ACG	CTT	CCC	3071
Cys	*	Thr	Arg	Pro	Gly	Pro	Gly	Ala	Arg	Ala	Arg	Val	Thr	Leu	Pro	
	1010					1015						1020				
TGC	CCA	GCT	CCG	TGG	CCG	AGG	CCT	TCG	CTC	GGC	CCA	GCT	CGC	TGC	CCG	3119
Cys	Pro	Ala	Pro	Trp	Pro	Arg	Pro	Ser	Leu	Gly	Pro	Ala	Arg	Cys	Pro	
	1025				1030						1035					
CTG	GGT	GCA	CCG	GCC	CCG	CCT	GCG	CCC	GCC	CCG	ACG	GCC	ACT	CGG	CCT	3167
Leu	Gly	Ala	Pro	Ala	Pro	Pro	Ala	Pro	Ala	Pro	Thr	Ala	Thr	Arg	Pro	
1040				1045				1050						1055		
GCA	GGC	GCT	TGG	CGC	AGG	CGC	AGT	CGA	TGT	GCT	TGC	CGA	TCT	ACC	GGG	3215
Ala	Gly	Ala	Trp	Arg	Arg	Arg	Ser	Arg	Cys	Ala	Cys	Arg	Ser	Thr	Gly	
			1060					1065					1070			
AGG	CCT	GCC	AGG	AGG	GCG	AGC	AGG	CAG	GGG	CCC	CCG	CCT	GGC	AGC	ACA	3263
Arg	Pro	Ala	Arg	Arg	Ala	Ser	Arg	Gln	Gly	Pro	Pro	Pro	Gly	Ser	Thr	
		1075						1080					1085			

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GAC AGC ACG TCT GCC TGC ACG CCC ACG CCC ACC TGC CAT TGT GCT GGG	3311
Asp Ser Thr Ser Ala Cys Thr Pro Thr Pro Thr Cys His Cys Ala Gly	
1090 1095 1100	
GGG CTG TCT GTC CTC ACC TTC CAC CCT GTG ACA GCC ACG GCT CCT GGC	3359
Gly Leu Ser Val Leu Thr Phe His Pro Val Thr Ala Thr Ala Pro Gly	
1105 1110 1115	
TCT CCG GCG CCT GGG GGC CTC TGG GGC ACA GCG GCA GGA CTC TGG GGC	3407
Ser Pro Ala Pro Gly Gly Leu Trp Gly Thr Ala Ala Gly Leu Trp Gly	
1120 1125 1130 1135	
TGG GCA CAG GCT ACA GAG ACA GTG GGG GAC TGG ACG AGA TCA GCA GTG	3455
Trp Ala Gln Ala Thr Glu Thr Val Gly Asp Trp Thr Arg Ser Ala Val	
1140 1145 1150	
TAG CCC GTG GGA CGC AAG GCT TCC CGG GAC CCT GCA CCT GGA GAC GGA	3503
* Pro Val Gly Arg Lys Ala Ser Arg Asp Pro Ala Pro Gly Asp Gly	
1155 1160 1165	
TCT CCA GTC TGG AGT CAG AAG TGT GAG TTA TCA GCC ACT CAG GCT CCG	3551
Ser Pro Val Trp Ser Gln Lys Cys Glu Leu Ser Ala Thr Gln Ala Pro	
1170 1175 1180	
AGC CAG CTG GAT TCT CTG CCT GCC ACT GTC AGG GTT AAG CGG CAG GCA	3599
Ser Gln Leu Asp Ser Leu Pro Ala Thr Val Arg Val Lys Arg Gln Ala	
1185 1190 1195	
GGA TTG GCC CTT CTC TGG CTT CTA CCA TGA AAT CCT GGC CAT GGC ACC	3647
Gly Leu Ala Leu Leu Trp Leu Leu Pro * Asn Pro Gly His Gly Thr	
1200 1205 1210 1215	
CCA GTG ACA GAT GAT GTC TTC CAT GGT CAT CAG TGA CCT CAG CTA GCC	3695
Pro Val Thr Asp Asp Val Phe His Gly His Gln * Pro Gln Leu Ala	
1220 1225 1230	
TCA	3698
Ser	

## (2) INFORMATION FOR SEQ ID NO:44:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...3243

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC GAG GCG	48
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala	
1 5 10 15	
GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG CCC AAC	96
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn	
20 25 30	
CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC GTG GGC	144

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Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	
	35						40					45				
CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	CAG	AAG	192
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	
	50					55					60					
GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	TAC	TGG	240
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	
65					70					75					80	
CGC	CAG	CAT	GGA	ACC	CAG	AAG	GGG	GTG	TGC	CAG	CCC	CGG	CCG	GGG	ACT	288
Arg	Gln	His	Gly	Thr	Gln	Lys	Gly	Val	Cys	Gln	Pro	Arg	Pro	Gly	Thr	
				85					90					95		
GCC	GTG	TTC	ACC	CTG	GGC	CCG	TCA	GCC	CTG	CCC	GGG	AGG	CCT	TCT	ACA	336
Ala	Val	Phe	Thr	Leu	Gly	Pro	Ser	Ala	Leu	Pro	Gly	Arg	Pro	Ser	Thr	
			100					105					110			
GGC	ACC	TAC	TGA	ATG	TCA	CCT	GGG	AGG	GCC	GAG	ACT	TCT	CCT	TCA	GCC	384
Gly	Thr	Tyr	*	Met	Ser	Pro	Gly	Arg	Ala	Glu	Thr	Ser	Pro	Ser	Ala	
		115					120					125				
CTG	GTG	GGT	ACC	TGG	TCC	AGC	CCA	CCA	TGG	TGG	TGA	TCG	CCC	TCA	ACC	432
Leu	Val	Gly	Thr	Trp	Ser	Ser	Pro	Pro	Trp	Trp	*	Ser	Pro	Ser	Thr	
	130					135					140					
GGC	ACC	GCC	TCT	GGG	AGA	TGG	TGG	GGC	GCT	GGG	AGC	ATG	GCG	TCC	TAT	480
Gly	Thr	Ala	Ser	Gly	Arg	Trp	Trp	Gly	Ala	Gly	Ser	Met	Ala	Ser	Tyr	
145					150					155					160	
ACA	TGA	AGT	ACC	CCG	TGT	GGC	CTC	GCT	ACA	GTG	CCT	CTC	TGC	AGC	CTG	528
Thr	*	Ser	Thr	Pro	Cys	Gly	Leu	Ala	Thr	Val	Pro	Leu	Cys	Ser	Leu	
				165					170					175		
TGG	TGG	ACA	GTC	GGC	ACC	TGA	CGG	TGG	CCA	CGC	TGG	AAG	AGC	GGC	CCT	576
Trp	Trp	Thr	Val	Gly	Thr	*	Arg	Trp	Pro	Arg	Trp	Lys	Ser	Gly	Pro	
			180					185					190			
TTG	TCA	TCG	TGG	AGA	GCC	CTG	ACC	CTG	GCA	CAG	GAG	GCT	GTG	TCC	CCA	624
Leu	Ser	Ser	Trp	Arg	Ala	Leu	Thr	Leu	Ala	Gln	Glu	Ala	Val	Ser	Pro	
		195					200					205				
ACA	CCG	TGC	CCT	GCC	GCA	GGC	AGA	GCA	ACC	ACA	CCT	TCA	GCA	GCG	GGG	672
Thr	Pro	Cys	Pro	Ala	Ala	Gly	Arg	Ala	Thr	Thr	Pro	Ser	Ala	Ala	Gly	
	210					215					220					
ACG	TGG	CCC	CCT	ACA	CCA	AGC	TCT	GCT	GTA	AGG	GAT	TCT	GCA	TCG	ACA	720
Thr	Trp	Pro	Pro	Thr	Pro	Ser	Ser	Ala	Val	Arg	Asp	Ser	Ala	Ser	Thr	
225					230					235					240	
TCC	TCA	AGA	AGC	TGG	CCA	GAG	TGG	TCA	AAT	TCT	CCT	ACG	ACC	TGT	ACC	768
Ser	Ser	Arg	Ser	Trp	Pro	Glu	Trp	Ser	Asn	Ser	Pro	Thr	Thr	Cys	Thr	
				245					250					255		
TGG	TGA	CCA	ACG	GCA	AGC	ATG	GCA	AGC	GGG	TGC	GCG	GCG	TAT	GGA	ACG	816
Trp	*	Pro	Thr	Ala	Ser	Met	Ala	Ser	Gly	Cys	Ala	Ala	Tyr	Gly	Thr	
			260					265					270			
GCA	TGA	TTG	GGG	AGG	TGT	ACT	ACA	AGC	GGG	CAG	ACA	TGG	CCA	TCG	GCT	864
Ala	*	Leu	Gly	Arg	Cys	Thr	Thr	Ser	Gly	Gln	Thr	Trp	Pro	Ser	Ala	
		275					280					285				
CCC	TCA	CCA	TCA	ATG	AGG	AAC	GCT	CCG	AGA	TCG	TAG	ACT	TCT	CTG	TAC	912
Pro	Ser	Pro	Ser	Met	Arg	Asn	Ala	Pro	Arg	Ser	*	Thr	Ser	Leu	Tyr	
	290					295					300					



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CCT Pro 305	TTG Leu	TGG Trp	AGA Arg	CGG Arg	GCA Ala 310	TCA Ser	GTG Val	TGA *	TGG Trp	TGG Trp 315	CTC Leu	GCA Ala	GCA Ala	ATG Met	GCA Ala 320	960
CCG Pro	TCT Ser	CCC Pro	CCT Pro	CGG Arg 325	CCT Pro	TCT Ser	TGG Trp	AGC Ser	CAT His 330	ATA Ile	GCC Ala	CTG Leu	CAG Gln	TGT Cys 335	GGG Gly	1008
TGA *	TGA *	TGT Cys	TTG Leu 340	TCA Ser	TGT Cys	GCC Ala	TCA Ser	CTG Leu 345	TGG Trp	TGG Trp	CCA Pro	TCA Ser	CCG Pro 350	TCT Ser	TCA Ser	1056
TGT Cys	TCG Ser	AGT Ser 355	ACT Thr	TCA Ser	GCC Ala	CTG Leu	TCA Ser 360	GCT Ala	ACA Thr	ACC Thr	AGA Arg	ACC Thr 365	TCA Ser	CCA Pro	GAG Glu	1104
GCA Ala 370	AGA Arg	AGT Ser	CCG Pro	GGG Gly	GCC Ala	CAG Gln 375	CTT Leu	TCA Ser	CTA Leu	TCG Ser	GCA Ala 380	AGT Ser	CCG Pro	TGT Cys	GGC Gly	1152
TGC Cys 385	TGT Cys	GGG Gly	CGC Arg	TGG Trp	TCT Ser 390	TCA Ser	ACA Thr	ACT Thr	CAG Gln	TGC Cys 395	CCA Pro	TCG Ser	AGA Arg	ACC Thr	CGC Arg 400	1200
GGG Gly	GCA Ala	CCA Pro	CCA Pro	GCA Ala 405	AGA Arg	TCA Ser	TGG Trp	TTC Phe	TGG Trp 410	TCT Ser	GGG Gly	CCT Pro	TCT Ser	TTG Leu 415	CTG Leu	1248
TCA Ser	TCT Ser	TCC Ser	TCG Ser 420	CCA Pro	GAT Asp	ACA Thr	CGG Arg	CCA Pro 425	ACC Thr	TGG Trp	CCG Pro	CCT Pro	TCA Ser 430	TGA *	TCC Ser	1296
AAG Lys	AGC Ser	AAT Asn 435	ACA Thr	TCG Ser	ACA Thr	CTG Leu	TGT Cys 440	CGG Arg	GCC Ala	TCA Ser	GTG Val	ACA Thr 445	AGA Arg	AGT Ser	TTC Phe	1344
AGC Ser 450	GGC Gly	CTC Leu	AAG Lys	ATC Ile	AGT Ser	ACC Ser 455	CAC His	CTT Leu	TCC Ser	GCT Ala	TCG Ser 460	GCA Ala	CGG Arg	TGC Cys	CCA Pro	1392
ACG Thr 465	GCA Ala	GCA Ala	CGG Arg	AGC Ser	GGA Gly 470	ACA Thr	TCC Ser	GCA Ala	GTA Val	ACT Thr 475	ACC Thr	GTG Val	ACA Thr	TGC Cys	ACA Thr 480	1440
CCC Pro	ACA Thr	TGG Trp	TCA Ser	AGT Ser 485	TCA Ser	ACC Thr	AGC Ser	GCT Ala	CGG Arg 490	TGG Trp	AGG Arg	ACG Thr	CGC Arg	TCA Ser 495	CCA Pro	1488
GCC Ala	TCA Ser	AGA Arg	TGG Trp 500	GCT Ala	CTG Leu	AGG Arg	CTC Leu	AGC Ser 505	CTG Leu	TCC Ser	CCA Pro	GGA Gly	AGC Ser 510	TGG Trp	ATG Met	1536
CCT Pro	TCA Ser	TCT Ser 515	ATG Met	ATG Met	CTG Leu	CTG Leu	TCC Ser 520	TCA Ser	ACT Thr	ACA Thr	TGG Trp	CAG Gln 525	GCA Ala	AGG Arg	ACG Thr	1584
AGG Arg 530	GCT Ala	GCA Ala	AGC Ser	TGG Trp	TCA Ser	CCA Pro 535	TTG Leu	GGT Gly	CTG Leu	GCA Ala	AGG Arg 540	TCT Ser	TTG Leu	CTA Leu	CCA Pro	1632
CTG Leu 545	GCT Ala	ACG Thr	GCA Ala	TCG Ser	CCA Pro 550	TGC Cys	AGA Arg	AGG Arg	ACT Thr	CCC Pro 555	ACT Thr	GGA Gly	AGC Ser	GGG Gly	CCA Pro 560	1680
TAG *	ACC Thr	TGG Trp	CGC Arg	TCT Ser 565	TGC Cys	AGT Ser	TCC Ser	TGG Trp	GGG Gly 570	ACG Thr	GAG Glu	AGA Arg	CAC His	AGA Arg 575	AAC Asn	1728

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TGG	AGA	CAG	TGT	GGC	TCT	CAG	GGA	TCT	GCC	AGA	ATG	AGA	AGA	ACG	AGG	1776
Trp	Arg	Gln	Cys	Gly	Ser	Gln	Gly	Ser	Ala	Arg	Met	Arg	Arg	Thr	Arg	
		580						585					590			
TGA	TGA	GCA	GCA	AGC	TGG	ACA	TCG	ACA	ACA	TGG	GAG	GCG	TCT	TCT	ACA	1824
*	*	Ala	Ala	Ser	Trp	Thr	Ser	Thr	Thr	Trp	Glu	Ala	Ser	Ser	Thr	
		595					600					605				
TGC	TGC	TGG	TGG	CCA	TGG	GGC	TGG	CCC	TGC	TGG	TCT	TCG	CCT	GGG	AGC	1872
Cys	Cys	Trp	Trp	Pro	Trp	Gly	Trp	Pro	Cys	Trp	Ser	Ser	Pro	Gly	Ser	
	610					615					620					
ACC	TGG	TCT	ACT	GGA	AGC	TGC	GCC	ACT	CGG	TGC	CCA	ACT	CAT	CCC	AGC	1920
Thr	Trp	Ser	Thr	Gly	Ser	Cys	Ala	Thr	Arg	Cys	Pro	Thr	His	Pro	Ser	
625					630					635					640	
TGG	ACT	TCC	TGC	TGG	CTT	TCA	GCA	GGG	GCA	TCT	ACA	GCT	GCT	TCA	GCG	1968
Trp	Thr	Ser	Cys	Trp	Leu	Ser	Ala	Gly	Ala	Ser	Thr	Ala	Ala	Ser	Ala	
				645					650						655	
GGG	TGC	AGA	GCC	TCG	CCA	GCC	CAC	CGC	GGC	AGG	CCA	GCC	CGG	ACC	TCA	2016
Gly	Cys	Arg	Ala	Ser	Pro	Ala	His	Arg	Gly	Arg	Pro	Ala	Arg	Thr	Ser	
			660					665					670			
CGG	CCA	GCT	CGG	CCC	AGG	CCA	GCG	TGC	TCA	AGA	TTC	TGC	AGG	CAG	CCC	2064
Arg	Pro	Ala	Arg	Pro	Arg	Pro	Ala	Cys	Ser	Arg	Phe	Cys	Arg	Gln	Pro	
		675					680						685			
GCG	ACA	TGG	TGA	CCA	CGG	CGG	GCG	TAA	GCA	ACT	CCC	TGG	ACC	GCG	CCA	2112
Ala	Thr	Trp	*	Pro	Arg	Arg	Ala	*	Ala	Thr	Pro	Trp	Thr	Ala	Pro	
	690					695					700					
CTC	GCA	CCA	TCG	AGA	ATT	GGG	GTG	GCG	GCC	GCC	GTG	CGC	CCC	CAC	CGT	2160
Leu	Ala	Pro	Ser	Arg	Ile	Gly	Val	Ala	Ala	Ala	Val	Arg	Pro	His	Arg	
705					710						715				720	
CCC	CCT	GCC	CGA	CCC	CGC	GGT	CTG	GCC	CCA	GCC	CAT	GCC	TGC	CCA	CCC	2208
Pro	Pro	Ala	Arg	Pro	Arg	Gly	Leu	Ala	Pro	Ala	His	Ala	Cys	Pro	Pro	
				725					730					735		
CCG	ACC	CGC	CCC	CAG	AGC	CGA	GCC	CCA	CGG	GCT	GGG	GAC	CGC	CAG	ACG	2256
Pro	Thr	Arg	Pro	Gln	Ser	Arg	Ala	Pro	Arg	Ala	Gly	Asp	Arg	Gln	Thr	
			740					745					750			
GGG	GTC	GCG	CGG	CGC	TTG	TGC	GCA	GGG	CTC	CGC	AGC	CCC	CGG	GCC	GCC	2304
Gly	Val	Ala	Arg	Arg	Leu	Cys	Ala	Gly	Leu	Arg	Ser	Pro	Arg	Ala	Ala	
	755						760					765				
CCC	CGA	CGC	CGG	GGC	CGC	CCC	TGT	CCG	ACG	TCT	CCC	GAG	TGT	CGC	GCC	2352
Pro	Arg	Arg	Arg	Gly	Arg	Pro	Cys	Pro	Thr	Ser	Pro	Glu	Cys	Arg	Ala	
	770					775					780					
GCC	CAG	CCT	GGG	AGG	CGC	GGT	GGC	CGG	TGC	GGA	CCG	GGC	ACT	GCG	GGA	2400
Ala	Gln	Pro	Gly	Arg	Arg	Gly	Gly	Arg	Cys	Gly	Pro	Gly	Thr	Ala	Gly	
785					790				795						800	
GGC	ACC	TCT	CGG	CCT	CCG	AGC	GGC	CCC	TGT	CGC	CCG	CGC	GCT	GTC	ACT	2448
Gly	Thr	Ser	Arg	Pro	Pro	Ser	Gly	Pro	Cys	Arg	Pro	Arg	Ala	Val	Thr	
				805					810					815		
ACA	GCT	CCT	TTC	CTC	GAG	CCG	ACC	GAT	CCG	GCC	GCC	CCT	TCC	TCC	CGC	2496
Thr	Ala	Pro	Phe	Leu	Glu	Pro	Thr	Asp	Pro	Ala	Ala	Pro	Ser	Ser	Arg	
			820					825					830			
TCT	TCC	CGG	AGC	CCC	CGG	AGC	TGG	AGG	ACC	TGC	CGC	TGC	TCG	GTC	CGG	2544
Ser	Ser	Arg	Ser	Pro	Arg	Ser	Trp	Arg	Thr	Cys	Arg	Cys	Ser	Val	Arg	
		835					840					845				

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AGC Ser	AGC Ser	TGG Trp	CCC Pro	GGC Gly	GGG Gly	AGG Arg	CCC Pro	TGC Cys	TGA *	ACG Thr	CGG Arg	CCT Pro	GGG Gly	CCC Pro	GGG Gly	2592
850						855					860					
GCT Ala	CGC Arg	GCC Ala	CGA Arg	GTC Val	ACG Thr	CTT Leu	CCC Pro	TGC Cys	CCA Pro	GCT Ala	CCG Pro	TGG Trp	CCG Pro	AGG Arg	CCT Pro	2640
865					870					875					880	
TCG Ser	CTC Leu	GGC Gly	CCA Pro	GCT Ala	CGC Arg	TGC Cys	CCG Pro	CTG Leu	GGT Gly	GCA Ala	CCG Pro	GCC Ala	CCG Pro	CCT Pro	GCG Ala	2688
				885					890					895		
CCC Pro	GCC Ala	CCG Pro	ACG Thr	GCC Ala	ACT Thr	CGG Arg	CCT Pro	GCA Ala	GGC Gly	GCT Ala	TGG Trp	CGC Arg	AGG Arg	CGC Arg	AGT Ser	2736
			900					905					910			
CGA Arg	TGT Cys	GCT Ala	TGC Cys	CGA Arg	TCT Ser	ACC Thr	GGG Gly	AGG Arg	CCT Pro	GCC Ala	AGG Arg	AGG Arg	GCG Ala	AGC Ser	AGG Arg	2784
		915					920					925				
CAG Gln	GGG Gly	CCC Pro	CCG Pro	CCT Pro	GGC Gly	AGC Ser	ACA Thr	GAC Asp	AGC Ser	ACG Thr	TCT Ser	GCC Ala	TGC Cys	ACG Thr	CCC Pro	2832
	930					935					940					
ACG Thr	CCC Pro	ACC Thr	TGC Cys	CAT His	TGT Cys	GCT Ala	GGG Gly	GGG Gly	CTG Leu	TCT Ser	GTC Val	CTC Leu	ACC Thr	TTC Phe	CAC His	2880
945					950					955					960	
CCT Pro	GTG Val	ACA Thr	GCC Ala	ACG Thr	GCT Ala	CCT Pro	GGC Gly	TCT Ser	CCG Pro	GCG Ala	CCT Pro	GGG Gly	GGC Gly	CTC Leu	TGG Trp	2928
				965					970					975		
GGC Gly	ACA Thr	GCG Ala	GCA Ala	GGA Gly	CTC Leu	TGG Trp	GGC Gly	TGG Trp	GCA Ala	CAG Gln	GCT Ala	ACA Thr	GAG Glu	ACA Thr	GTG Val	2976
			980				985						990			
GGG Gly	GAC Asp	TGG Trp	ACG Thr	AGA Arg	TCA Ser	GCA Ala	GTG Val	TAG *	CCC Pro	GTG Val	GGA Gly	CGC Arg	AAG Lys	GCT Ala	TCC Ser	3024
		995				1000					1005					
CGG Arg	GAC Asp	CCT Pro	GCA Ala	CCT Pro	GGA Gly	GAC Asp	GGA Gly	TCT Ser	CCA Pro	GTC Val	TGG Trp	AGT Ser	CAG Gln	AAG Lys	TGT Cys	3072
	1010				1015					1020						
GAG Glu	TTA Leu	TCA Ser	GCC Ala	ACT Thr	CAG Gln	GCT Ala	CCG Pro	AGC Ser	CAG Gln	CTG Leu	GAT Asp	TCT Ser	CTG Leu	CCT Pro	GCC Ala	3120
1025					1030				1035					1040		
ACT Thr	GTC Val	AGG Arg	GTT Val	AAG Lys	CGG Arg	CAG Gln	GCA Ala	GGA Gly	TTG Leu	GCC Ala	CTT Leu	CTC Leu	TGG Trp	CTT Leu	CTA Leu	3168
				1045				1050				1055				
CCA Pro	TGA *	AAT Asn	CCT Pro	GGC Gly	CAT His	GGC Gly	ACC Thr	CCA Pro	GTG Val	ACA Thr	GAT Asp	GAT Asp	GTC Val	TTC Phe	CAT His	3216
			1060				1065						1070			
GGT Gly	CAT His	CAG Gln	TGA *	CCT Pro	CAG Gln	CTA Leu	GCC Ala	TCA Ser								3243
		1075				1080										

## (2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4092 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both

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(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 189..3923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806

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Val	Ser	Trp	Arg	Leu 195	Leu	Asp	Val	Val	Thr 200	Leu	Glu	Leu	Asp	Pro 205	Gly	
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu 215	Leu	Arg	Gln	Leu	Asp 220	Ala	Pro	
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu 230	Glu	Ala	Glu	Val	Leu 235	Phe	Ala	
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly 245	Pro	Gly	His	Val	Trp	Leu	Val	
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly 260	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro 270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu 280	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile 295	Leu	Ala	Leu	Gly	Ala	His	Ser	
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu 310	Pro	Ala	Pro	Ala	Gly 315	Asp	Cys	Arg	
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro 325	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly 340	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly 350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met 355	Val	Val	Ile	Ala	Leu	Asn	Arg	His 365	
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg 375	Trp	Glu	His	Gly	Val	Leu 380	Tyr	Met	
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr 390	Ser	Ala	Ser	Leu	Gln 395	Pro	Val	Val	
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala 405	Thr	Leu	Glu	Glu	Arg 410	Pro	Phe	Val	
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp 420	Pro	Gly	Thr	Gly	Gly 425	Cys	Val	Pro	Asn	Thr 430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn 435	His	Thr	Phe	Ser	Ser	Gly 445	Asp	Val	
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys 455	Lys	Gly	Phe	Cys	Ile	Asp 460	Ile	Leu	

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AAG Lys	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu	TAC Tyr	CTG Leu	GTG Val	1622
		465					470					475				
ACC Thr	AAC Asn	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys	CGG Arg	GTG Val	CGC Arg	GGC Gly	GTA Val	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
	480					485					490					
ATT Ile	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu	1718
	495				500					505					510	
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro	TTT Phe	1766
				515					520					525		
GTG Val	GAG Glu	ACG Thr	GGC Gly	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly	ACC Thr	GTC Val	1814
			530					535					540			
TCC Ser	CCC Pro	TCG Ser	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro	TAT Tyr	AGC Ser	CCT Pro	GCA Ala	GTG Val	TGG Trp	GTG Val	ATG Met	1862
		545					550					555				
ATG Met	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
	560					565					570					
GAG Glu	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys	1958
	575				580				585						590	
AAG Lys	TCC Ser	GGG Gly	GGC Gly	CCA Pro	GCT Ala	TTC Phe	ACT Thr	ATC Ile	GGC Gly	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu	CTG Leu	2006
				595					600					605		
TGG Trp	GCG Ala	CTG Leu	GTC Val	TTC Phe	AAC Asn	AAC Asn	TCA Ser	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro	CGG Arg	GGC Gly	2054
			610					615					620			
ACC Thr	ACC Thr	AGC Ser	AAG Lys	ATC Ile	ATG Met	GTT Val	CTG Leu	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val	ATC Ile	2102
		625					630					635				
TTC Phe	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	ACG Thr	GCC Ala	AAC Asn	CTG Leu	GCC Ala	GCC Ala	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	2150
	640					645					650					
CAA Gln	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	GTG Val	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg	2198
	655				660					665					670	
CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr	CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn	GGC Gly	2246
				675					680					685		
AGC Ser	ACG Thr	GAG Glu	CGG Arg	AAC Asn	ATC Ile	CGC Arg	AGT Ser	AAC Asn	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His	ACC Thr	CAC His	2294
			690					695					700			
ATG Met	GTC Val	AAG Lys	TTC Phe	AAC Asn	CAG Gln	CGC Arg	TCG Ser	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu	ACC Thr	AGC Ser	CTC Leu	2342
		705					710					715				
AAG Lys	ATG Met	GGC Gly	TCT Ser	GAG Glu	GCT Ala	CAG Gln	CCT Pro	GTC Val	CCC Pro	AGG Arg	AAG Lys	CTG Leu	GAT Asp	GCC Ala	TTC Phe	2390
	720					725					730					

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ATC Ile 735	TAT Tyr	GAT Asp	GCT Ala	GCT Ala	GTC Val 740	CTC Leu	AAC Asn	TAC Tyr	ATG Met	GCA Ala 745	GGC Gly	AAG Lys	GAC Asp	GAG Glu	GGC Gly 750	2438
TGC Cys	AAG Lys	CTG Leu	GTC Val	ACC Thr 755	ATT Ile	GGG Gly	TCT Ser	GGC Gly	AAG Lys 760	GTC Val	TTT Phe	GCT Ala	ACC Thr	ACT Thr	GGC Gly 765	2486
TAC Tyr	GGC Gly	ATC Ile	GCC Ala 770	ATG Met	CAG Gln	AAG Lys	GAC Asp	TCC Ser 775	CAC His	TGG Trp	AAG Lys	CGG Arg	GCC Ala 780	ATA Ile	GAC Asp	2534
CTG Leu	GCG Ala	CTC Leu	TTG Leu	CAG Gln	TTC Phe	CTG Leu	GGG Gly 790	GAC Asp	GGA Gly	GAG Glu	ACA Thr	CAG Gln	AAA Lys	CTG Leu	GAG Glu	2582
ACA Thr 800	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly	ATC Ile 805	TGC Cys	CAG Gln	AAT Asn	GAG Glu	AAG Lys 810	AAC Asn	GAG Glu	GTG Val	ATG Met	2630
AGC Ser 815	AGC Ser	AAG Lys	CTG Leu	GAC Asp	ATC Ile 820	GAC Asp	AAC Asn	ATG Met	GGA Gly	GGC Gly	GTC Val	TTC Phe	TAC Tyr	ATG Met	CTG Leu 830	2678
CTG Leu	GTG Val	GCC Ala	ATG Met	GGG Gly 835	CTG Leu	GCC Ala	CTG Leu	CTG Leu	GTC Val 840	TTC Phe	GCC Ala	TGG Trp	GAG Glu	CAC His	CTG Leu 845	2726
GTC Val	TAC Tyr	TGG Trp	AAG Lys 850	CTG Leu	CGC Arg	CAC His	TCG Ser	GTG Val 855	CCC Pro	AAC Asn	TCA Ser	TCC Ser	CAG Gln	CTG Leu	GAC Asp 860	2774
TTC Phe	CTG Leu	CTG Leu	GCT Ala	TTC Phe	AGC Ser	AGG Arg	GGC Gly 870	ATC Ile	TAC Tyr	AGC Ser	TGC Cys	TTC Phe	AGC Ser	GGG Gly	GTG Val	2822
CAG Gln 880	AGC Ser	CTC Leu	GCC Ala	AGC Ser	CCA Pro	CCG Pro	CGG Arg 885	CAG Gln	GCC Ala	AGC Ser	CCG Pro	GAC Asp	CTC Leu	ACG Thr	GCC Ala	2870
AGC Ser 895	TCG Ser	GCC Ala	CAG Gln	GCC Ala	AGC Ser	GTG Val	CTC Leu	AAG Lys	ATT Ile	CTG Leu	CAG Gln	GCA Ala	GCC Ala	CGC Arg	GAC Asp 910	2918
ATG Met	GTG Val	ACC Thr	ACG Thr	GCG Ala	GGC Gly	GTA Val	AGC Ser	AAC Asn	TCC Ser	CTG Leu	GAC Asp	CGC Arg	GCC Ala	ACT Thr	CGC Arg 925	2966
ACC Thr	ATC Ile	GAG Glu	AAT Asn	TGG Trp	GGT Gly	GGC Gly	GGC Gly	CGC Arg	CGT Arg	GCG Ala	CCC Pro	CCA Pro	CCG Pro	TCC Ser	CCC Pro	3014
TGC Cys	CCG Pro	ACC Thr	CCG Pro	CGG Arg	TCT Ser	GGC Gly	CCC Pro	AGC Ser	CCA Pro	TGC Cys	CTG Leu	CCC Pro	ACC Thr	CCC Pro	GAC Asp	3062
CCG Pro	CCC Pro	CCA Pro	GAG Glu	CCG Pro	AGC Ser	CCC Pro	ACG Thr	GGC Gly	TGG Trp	GGA Gly	CCG Pro	CCA Pro	GAC Asp	GGG Gly	GGT Gly	3110
CGC Arg 975	GCG Ala	GCG Ala	CTT Leu	GTG Val	CGC Arg	AGG Arg	GCT Ala	CCG Pro	CAG Gln	CCC Pro	CCG Pro	GGC Gly	CGC Arg	CCC Pro	CCG Pro 990	3158
ACG Thr	CCG Pro	GGG Gly	CCG Pro	CCC Pro	CTG Leu	TCC Ser	GAC Asp	GTC Val	TCC Ser	CGA Arg	GTG Val	TCG Ser	CGC Arg	CGC Arg	CCA Pro 1005	3206

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GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG AGG CAC Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His 1010 1015 1020	3254
CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser 1025 1030 1035	3302
TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG CTC TTC Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe 1040 1045 1050	3350
CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG GAG CAG Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln 1055 1060 1065 1070	3398
CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG GGC TCG Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser 1075 1080 1085	3446
CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC TTC GCT Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala 1090 1095 1100	3494
CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC GCC CGC Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg 1105 1110 1115	3542
CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG TCG ATG Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met 1120 1125 1130	3590
TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG GCA GGG Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly 1135 1140 1145 1150	3638
GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC CAC GCC Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala 1155 1160 1165	3686
CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA CCC TGT His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys 1170 1175 1180	3734
GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG GGG CAC Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His 1185 1190 1195	3782
AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT GGG GGA Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly 1200 1205 1210	3830
CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC CCG GGA Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly 1215 1220 1225 1230	3878
CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1235 1240 124	3930
GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG	3990
GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA	4050
GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4092



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## (2) INFORMATION FOR SEQ ID NO:46:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1           5           10           15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
          20           25           30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
          35           40           45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
 50           55           60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
 65           70           75           80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
          85           90           95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
          100          105          110
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
          115          120          125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
          130          135          140
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
          145          150          155          160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
          165          170          175
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
          180          185          190
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
          195          200          205
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
          210          215          220
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
          225          230          235          240
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
          245          250          255
Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
          260          265          270
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
          275          280          285
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp

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290					295					300					
Arg 305	Gln	His	Gly	Thr	Leu 310	Pro	Ala	Pro	Ala	Gly 315	Asp	Cys	Arg	Val	His 320
Pro	Gly	Pro	Val	Ser 325	Pro	Ala	Arg	Glu	Ala 330	Phe	Tyr	Arg	His	Leu 335	Leu
Asn	Val	Thr	Trp 340	Glu	Gly	Arg	Asp	Phe 345	Ser	Phe	Ser	Pro	Gly 350	Gly	Tyr
Leu	Val	Gln	Pro	Thr	Met	Val	Val 360	Ile	Ala	Leu	Asn	Arg 365	His	Arg	Leu
Trp	Glu 370	Met	Val	Gly	Arg	Trp 375	Glu	His	Gly	Val	Leu 380	Tyr	Met	Lys	Tyr
Pro 385	Val	Trp	Pro	Arg	Tyr 390	Ser	Ala	Ser	Leu	Gln 395	Pro	Val	Val	Asp	Ser 400
Arg	His	Leu	Thr	Val 405	Ala	Thr	Leu	Glu	Glu 410	Arg	Pro	Phe	Val	Ile 415	Val
Glu	Ser	Pro	Asp 420	Pro	Gly	Thr	Gly	Gly 425	Cys	Val	Pro	Asn	Thr 430	Val	Pro
Cys	Arg	Arg 435	Gln	Ser	Asn	His	Thr 440	Phe	Ser	Ser	Gly	Asp 445	Val	Ala	Pro
Tyr	Thr 450	Lys	Leu	Cys	Cys	Lys 455	Gly	Phe	Cys	Ile	Asp 460	Ile	Leu	Lys	Lys
Leu 465	Ala	Arg	Val	Val	Lys 470	Phe	Ser	Tyr	Asp	Leu 475	Tyr	Leu	Val	Thr	Asn 480
Gly	Lys	His	Gly	Lys 485	Arg	Val	Arg	Gly	Val 490	Trp	Asn	Gly	Met	Ile 495	Gly
Glu	Val	Tyr	Tyr 500	Lys	Arg	Ala	Asp	Met	Ala 505	Ile	Gly	Ser	Leu 510	Thr	Ile
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val 520	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu
Thr 530	Gly	Ile	Ser	Val	Met	Val 535	Ala	Arg	Ser	Asn	Gly 540	Thr	Val	Ser	Pro
Ser 545	Ala	Phe	Leu	Glu	Pro	Tyr 550	Ser	Pro	Ala	Val 555	Trp	Val	Met	Met	Phe 560
Val	Met	Cys	Leu	Thr 565	Val	Val	Ala	Ile	Thr 570	Val	Phe	Met	Phe	Glu	Tyr 575
Phe	Ser	Pro	Val 580	Ser	Tyr	Asn	Gln	Asn 585	Leu	Thr	Arg	Gly	Lys 590	Lys	Ser
Gly	Gly	Pro 595	Ala	Phe	Thr	Ile	Gly 600	Lys	Ser	Val	Trp	Leu 605	Leu	Trp	Ala
Leu 610	Val	Phe	Asn	Asn	Ser	Val 615	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr
Ser 625	Lys	Ile	Met	Val	Leu	Val 630	Trp	Ala	Phe	Phe 635	Ala	Val	Ile	Phe	Leu 640
Ala	Arg	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr

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645					650					655					
Ile	Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln
			660					665					670		
Asp	Gln	Tyr	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr
		675					680					685			
Glu	Arg	Asn	Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val
	690					695					700				
Lys	Phe	Asn	Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met
	705					710					715				720
Gly	Ser	Glu	Ala	Gln	Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr
				725					730					735	
Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys
			740					745					750		
Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly
		755					760						765		
Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala
	770					775					780				
Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val
	785					790					795				800
Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser
				805					810					815	
Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val
			820					825					830		
Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr
		835					840					845			
Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu
	850					855					860				
Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser
	865					870					875				880
Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser
				885					890					895	
Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val
			900					905					910		
Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile
		915					920					925			
Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro
	930					935					940				
Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro
	945					950					955			960	
Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala
				965					970					975	
Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro
			980				985						990		
Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp

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995	1000	1005
Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser 1010 1015 1020		
Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe 1025 1030 1035 1040		
Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu 1045 1050 1055		
Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala 1060 1065 1070		
Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro 1075 1080 1085		
Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro 1090 1095 1100		
Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp 1105 1110 1115 1120		
Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu 1125 1130 1135		
Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro 1140 1145 1150		
Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala His Leu 1155 1160 1165		
Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser 1170 1175 1180		
His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly 1185 1190 1195 1200		
Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp 1205 1210 1215		
Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys 1220 1225 1230		
Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1235 1240		

## (2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4053 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	806
195 200 205	
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	854
210 215 220	
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	902
225 230 235	

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GAG Glu 240	GCG Ala 240	GCG Ala 240	CAG Gln 240	GCC Ala 240	GGT Gly 245	CTG Leu 245	GTG Val 245	GGG Gly 245	CCC Pro 245	GGC Gly 250	CAC His 250	GTG Val 250	TGG Trp 250	CTG Leu 250	GTG Val 250	950
CCC Pro 255	AAC Asn 255	CTG Leu 255	GCG Ala 255	CTG Leu 255	GGC Gly 260	AGC Ser 260	ACC Thr 260	GAT Asp 260	GCG Ala 265	CCC Pro 265	CCC Pro 265	GCC Ala 265	ACC Thr 265	TTC Phe 270	CCC Pro 270	998
GTG Val 275	GGC Gly 275	CTC Leu 275	ATC Ile 275	AGC Ser 275	GTC Val 275	GTC Val 275	ACC Thr 275	GAG Glu 280	AGC Ser 280	TGG Trp 280	CGC Arg 280	CTC Leu 285	AGC Ser 285	CTG Leu 285	CGC Arg 285	1046
CAG Gln 290	AAG Lys 290	GTG Val 290	CGC Arg 290	GAC Asp 290	GGC Gly 290	GTG Val 290	GCC Ala 295	ATT Ile 295	CTG Leu 295	GCC Ala 295	CTG Leu 295	GGC Gly 300	GCC Ala 300	CAC His 300	AGC Ser 300	1094
TAC Tyr 305	TGG Trp 305	CGC Arg 305	CAG Gln 305	CAT His 305	GGA Gly 310	ACC Thr 310	CTG Leu 310	CCA Pro 310	GCC Ala 310	CCG Pro 310	GCC Ala 315	GGG Gly 315	GAC Asp 315	TGC Cys 315	CGT Arg 315	1142
GTT Val 320	CAC His 320	CCT Pro 320	GGG Gly 320	CCC Pro 320	GTC Val 325	AGC Ser 325	CCT Pro 325	GCC Ala 325	CGG Arg 325	GAG Glu 330	GCC Ala 330	TTC Phe 330	TAC Tyr 330	AGG Arg 330	CAC His 330	1190
CTA Leu 335	CTG Leu 335	AAT Asn 335	GTC Val 335	ACC Thr 335	TGG Trp 340	GAG Glu 340	GGC Gly 340	CGA Arg 340	GAC Asp 345	TTC Phe 345	TCC Ser 345	TTC Phe 345	AGC Ser 345	CCT Pro 345	GGT Gly 350	1238
GGG Gly 355	TAC Tyr 355	CTG Leu 355	GTC Val 355	CAG Gln 355	CCC Pro 355	ACC Thr 355	ATG Met 355	GTG Val 360	GTG Val 360	ATC Ile 360	GCC Ala 360	CTC Leu 360	AAC Asn 365	CGG Arg 365	CAC His 365	1286
CGC Arg 370	CTC Leu 370	TGG Trp 370	GAG Glu 370	ATG Met 370	GTG Val 370	GGG Gly 370	CGC Arg 375	TGG Trp 375	GAG Glu 375	CAT His 375	GGC Gly 375	GTC Val 375	CTA Leu 380	TAC Tyr 380	ATG Met 380	1334
AAG Lys 385	TAC Tyr 385	CCC Pro 385	GTG Val 385	TGG Trp 385	CCT Pro 385	CGC Arg 385	TAC Tyr 390	AGT Ser 390	GCC Ala 390	TCT Ser 390	CTG Leu 395	CAG Gln 395	CCT Pro 395	GTG Val 395	GTG Val 395	1382
GAC Asp 400	AGT Ser 400	CGG Arg 400	CAC His 400	CTG Leu 400	ACG Thr 405	GTG Val 405	GCC Ala 405	ACG Thr 405	CTG Leu 410	GAA Glu 410	GAG Glu 410	CGG Arg 410	CCC Pro 410	TTT Phe 410	GTC Val 410	1430
ATC Ile 415	GTG Val 415	GAG Glu 415	AGC Ser 415	CCT Pro 415	GAC Asp 420	CCT Pro 420	GGC Gly 420	ACA Thr 420	GGA Gly 425	GGC Gly 425	TGT Cys 425	GTC Val 425	CCC Pro 425	AAC Asn 425	ACC Thr 430	1478
GTG Val 435	CCC Pro 435	TGC Cys 435	CGC Arg 435	AGG Arg 435	CAG Gln 435	AGC Ser 435	AAC Asn 435	CAC His 435	ACC Thr 440	TTC Phe 440	AGC Ser 440	AGC Ser 440	GGG Gly 445	GAC Asp 445	GTG Val 445	1526
GCC Ala 450	CCC Pro 450	TAC Tyr 450	ACC Thr 450	AAG Lys 450	CTC Leu 450	TGC Cys 450	TGT Cys 455	AAG Lys 455	GGA Gly 455	TTC Phe 455	TGC Cys 455	ATC Ile 460	GAC Asp 460	ATC Ile 460	CTC Leu 460	1574
AAG Lys 465	AAG Lys 465	CTG Leu 465	GCC Ala 465	AGA Arg 465	GTG Val 465	GTC Val 465	AAA Lys 470	TTC Phe 470	TCC Ser 470	TAC Tyr 475	GAC Asp 475	CTG Leu 475	TAC Tyr 475	CTG Leu 475	GTG Val 475	1622
ACC Thr 480	AAC Asn 480	GGC Gly 480	AAG Lys 480	CAT His 480	GGC Gly 485	AAG Lys 485	CGG Arg 485	GTG Val 485	CGC Arg 485	GGC Gly 490	GTA Val 490	TGG Trp 490	AAC Asn 490	GGC Gly 490	ATG Met 490	1670
ATT Ile 495	GGG Gly 495	GAG Glu 495	GTG Val 495	TAC Tyr 495	TAC Tyr 500	AAG Lys 500	CGG Arg 500	GCA Ala 500	GAC Asp 505	ATG Met 505	GCC Ala 505	ATC Ile 505	GGC Gly 505	TCC Ser 505	CTC Leu 510	1718

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ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
			515						520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530					535					540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
		545					550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
	560					565					570					
GAG	TAC	TTC	AGC	CCT	GTC	AGC	TAC	AAC	CAG	AAC	CTC	ACC	AGA	GGC	AAG	1958
Glu	Tyr	Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	
575					580				585						590	
ACT	TTC	ACT	ATC	GGC	AAG	TCC	GTG	TGG	CTG	CTG	TGG	GCG	CTG	GTC	TTC	2006
Thr	Phe	Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	
				595					600					605		
AAC	AAC	TCA	GTG	CCC	ATC	GAG	AAC	CCG	CGG	GGC	ACC	ACC	AGC	AAG	ATC	2054
Asn	Asn	Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	
			610					615					620			
ATG	GTT	CTG	GTC	TGG	GCC	TTC	TTT	GCT	GTC	ATC	TTC	CTC	GCC	AGA	TAC	2102
Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	
		625					630					635				
ACG	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAA	GAG	CAA	TAC	ATC	GAC	ACT	2150
Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	
	640					645					650					
GTG	TCG	GGC	CTC	AGT	GAC	AAG	AAG	TTT	CAG	CGG	CCT	CAA	GAT	CAG	TAC	2198
Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	
655					660				665						670	
CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	AGC	ACG	GAG	CGG	AAC	2246
Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	
				675					680					685		
ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	ATG	GTC	AAG	TTC	AAC	2294
Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	
			690				695						700			
CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	AAG	ATG	GGG	AAG	CTG	2342
Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Lys	Leu	
		705					710					715				
GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	GTC	CTC	AAC	TAC	ATG	GCA	GGC	AAG	2390
Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	
	720				725						730					
GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	ATT	GGG	TCT	GGC	AAG	GTC	TTT	GCT	2438
Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	
	735				740				745						750	
ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	2486
Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	
				755					760					765		
GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	2534
Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	
			770					775						780		

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AAA Lys	CTG Leu	GAG Glu	ACA Thr	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly	ATC Ile	TGC Cys	CAG Gln	AAT Asn	GAG Glu	AAG Lys	AAC Asn	2582
	785					790					795					
GAG Glu	GTG Val	ATG Met	AGC Ser	AGC Ser	AAG Lys	CTG Leu	GAC Asp	ATC Ile	GAC Asp	AAC Asn	ATG Met	GGA Gly	GGC Gly	GTC Val	TTC Phe	2630
	800					805					810					
TAC Tyr	ATG Met	CTG Leu	CTG Leu	GTG Val	GCC Ala	ATG Met	GGG Gly	CTG Leu	GCC Ala	CTG Leu	CTG Val	GTC Phe	TTC Ala	GCC Ala	TGG Trp	2678
	815				820					825					830	
GAG Glu	CAC His	CTG Leu	GTC Val	TAC Tyr	TGG Trp	AAG Lys	CTG Leu	CGC Arg	CAC His	TCG Ser	GTG Val	CCC Pro	AAC Asn	TCA Ser	TCC Ser	2726
				835					840					845		
CAG Gln	CTG Leu	GAC Asp	TTC Phe	CTG Leu	CTG Leu	GCT Ala	TTC Phe	AGC Ser	AGG Arg	GGC Gly	ATC Ile	TAC Tyr	AGC Ser	TGC Cys	TTC Phe	2774
			850					855					860			
AGC Ser	GGG Gly	GTG Val	CAG Gln	AGC Ser	CTC Leu	GCC Ala	AGC Ser	CCA Pro	CCG Pro	CGG Arg	CAG Gln	GCC Ala	AGC Ser	CCG Pro	GAC Asp	2822
		865					870					875				
CTC Leu	ACG Thr	GCC Ala	AGC Ser	TCG Ser	GCC Ala	CAG Gln	GCC Ala	AGC Ser	GTG Val	CTC Leu	AAG Lys	ATT Ile	CTG Leu	CAG Gln	GCA Ala	2870
	880					885					890					
GCC Ala	CGC Arg	GAC Asp	ATG Met	GTG Val	ACC Thr	ACG Thr	GCG Ala	GGC Gly	GTA Val	AGC Ser	AAC Asn	TCC Ser	CTG Leu	GAC Asp	CGC Arg	2918
	895				900					905					910	
GCC Ala	ACT Thr	CGC Arg	ACC Thr	ATC Ile	GAG Glu	AAT Asn	TGG Trp	GGT Gly	GGC Gly	GGC Gly	CGC Arg	CGT Arg	GCG Ala	CCC Pro	CCA Pro	2966
				915				920					925			
CCG Pro	TCC Ser	CCC Pro	TGC Cys	CCG Pro	ACC Thr	CCG Pro	CGG Arg	TCT Ser	GGC Gly	CCC Pro	AGC Ser	CCA Pro	TGC Cys	CTG Leu	CCC Pro	3014
			930					935					940			
ACC Thr	CCC Pro	GAC Asp	CCG Pro	CCC Pro	CCA Pro	GAG Glu	CCG Pro	AGC Ser	CCC Pro	ACG Thr	GGC Gly	TGG Trp	GGA Gly	CCG Pro	CCA Pro	3062
		945					950					955				
GAC Asp	GGG Gly	GGT Gly	CGC Arg	GCG Ala	GCG Ala	CTT Leu	GTG Val	CGC Arg	AGG Arg	GCT Ala	CCG Pro	CAG Gln	CCC Pro	CCG Pro	GGC Gly	3110
	960					965					970					
CGC Arg	CCC Pro	CCG Pro	ACG Thr	CCG Pro	GGG Gly	CCG Pro	CCC Pro	CTG Leu	TCC Ser	GAC Asp	GTC Val	TCC Ser	CGA Arg	GTG Val	TCG Ser	3158
	975				980					985					990	
CGC Arg	CGC Arg	CCA Pro	GCC Ala	TGG Trp	GAG Glu	GCG Ala	CGG Arg	TGG Trp	CCG Pro	GTG Val	CGG Arg	ACC Thr	GGG Gly	CAC His	TGC Cys	3206
				995				1000					1005			
GGG Gly	AGG Arg	CAC His	CTC Leu	TCG Ser	GCC Ala	TCC Ser	GAG Glu	CGG Arg	CCC Pro	CTG Leu	TCG Ser	CCC Pro	GCG Ala	CGC Arg	TGT Cys	3254
			1010					1015					1020			
CAC His	TAC Tyr	AGC Ser	TCC Ser	TTT Phe	CCT Pro	CGA Arg	GCC Ala	GAC Asp	CGA Arg	TCC Ser	GGC Gly	CGC Arg	CCC Pro	TTC Phe	CTC Leu	3302
			1025				1030					1035				
CCG Pro	CTC Leu	TTC Phe	CCG Pro	GAG Glu	CCC Pro	CCG Pro	GAG Glu	CTG Leu	GAG Glu	GAC Asp	CTG Leu	CCG Pro	CTG Leu	CTC Leu	GGT Gly	3350
	1040					1045					1050					



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CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC	3398
Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala	
1055 1060 1065 1070	
CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG	3446
Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu	
1075 1080 1085	
GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC	3494
Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala	
1090 1095 1100	
TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG	3542
Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala	
1105 1110 1115	
CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG	3590
Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu	
1120 1125 1130	
CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC	3638
Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His	
1135 1140 1145 1150	
GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT	3686
Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu	
1155 1160 1165	
CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT	3734
Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro	
1170 1175 1180	
CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC	3782
Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp	
1185 1190 1195	
AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC	3830
Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly	
1200 1205 1210	
TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA	3878
Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu	
1215 1220 1225 1230	
GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA	3931
Val	
CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG	3991
GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT	4051
CA	4053

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly

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1	5	10	15
Ala Trp Ala Gly 20	Leu Gly Pro Gly Gln 25	Gly Glu Gln Gly Met 30	Thr Val
Ala Val Val 35	Phe Ser Ser Ser Gly 40	Pro Pro Gln Ala Gln 45	Phe Arg Val
Arg Leu Thr 50	Pro Gln Ser Phe 55	Leu Asp Leu Pro Leu 60	Glu Ile Gln Pro
Leu Thr Val 65	Gly Val Asn Thr 70	Thr Asn Pro Ser 75	Ser Leu Leu Thr Gln 80
Ile Cys Gly 85	Leu Leu Gly Ala Ala 90	His Val His Gly 95	Ile Val Phe Glu
Asp Asn Val 100	Asp Thr Glu Ala Val 105	Gln Ile Leu Asp Phe 110	Ile Ser
Ser Gln Thr 115	His Val Pro Ile Leu 120	Ser Ile Ser Gly Gly 125	Ser Ala Val
Val Leu Thr 130	Pro Lys Glu Pro Gly 135	Ser Ala Phe Leu Gln 140	Leu Gly Val
Ser Leu Glu 145	Gln Gln Leu Gln Val 150	Leu Phe Lys Val 155	Leu Glu Glu Tyr 160
Asp Trp Ser 165	Ala Phe Ala Val Ile Thr 170	Ser Leu His Pro Gly 175	His Ala
Leu Phe Leu 180	Glu Gly Val Arg Ala Val 185	Ala Asp Ala Ser His 190	Val Ser
Trp Arg Leu 195	Leu Asp Val Val Thr 200	Leu Glu Leu Asp Pro 205	Gly Gly Pro
Arg Ala Arg 210	Thr Gln Arg Leu Leu Arg 215	Gln Leu Asp Ala Pro 220	Val Phe
Val Ala Tyr 225	Cys Ser Arg Glu Glu Ala Glu 230	Val Leu Phe Ala Glu 235	Ala 240
Ala Gln Ala 245	Gly Leu Val Gly Pro Gly 250	His Val Trp Leu Val Pro 255	Asn
Leu Ala Leu 260	Gly Ser Thr Asp Ala Pro 265	Pro Ala Thr Phe Pro 270	Val Gly
Leu Ile Ser 275	Val Val Thr Glu Ser Trp 280	Arg Leu Ser Leu Arg 285	Gln Lys
Val Arg Asp 290	Gly Val Ala Ile Leu Ala Leu Gly 295	Ala His Ser Tyr Trp 300	
Arg Gln His 305	Gly Thr Leu Pro Ala Pro Ala 310	Gly Asp Cys Arg Val 315	His 320
Pro Gly Pro 325	Val Ser Pro Ala Arg Glu Ala 330	Phe Tyr Arg His Leu 335	Leu
Asn Val Thr 340	Trp Glu Gly Arg Asp Phe 345	Ser Phe Ser Pro Gly 350	Gly Tyr
Leu Val Gln 355	Pro Thr Met Val Val Ile Ala Leu 360	Asn Arg His Arg Leu 365	

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355	360	365
Trp Glu Met Val Gly Arg	Trp Glu His Gly Val Leu	Tyr Met Lys Tyr
370	375	380
Pro Val Trp Pro Arg Tyr	Ser Ala Ser Leu Gln	Pro Val Val Asp Ser
385	390	395
Arg His Leu Thr Val Ala Thr	Leu Glu Glu Arg Pro Phe	Val Ile Val
405	410	415
Glu Ser Pro Asp Pro Gly Thr	Gly Gly Cys Val Pro Asn	Thr Val Pro
420	425	430
Cys Arg Arg Gln Ser Asn His	Thr Phe Ser Ser Gly Asp	Val Ala Pro
435	440	445
Tyr Thr Lys Leu Cys Cys Lys	Gly Phe Cys Ile Asp	Ile Leu Lys Lys
450	455	460
Leu Ala Arg Val Val Lys Phe	Ser Tyr Asp Leu Tyr	Leu Val Thr Asn
465	470	475
Gly Lys His Gly Lys Arg Val	Arg Gly Val Trp Asn	Gly Met Ile Gly
485	490	495
Glu Val Tyr Tyr Lys Arg Ala	Asp Met Ala Ile Gly	Ser Leu Thr Ile
500	505	510
Asn Glu Glu Arg Ser Glu Ile	Val Asp Phe Ser Val	Pro Phe Val Glu
515	520	525
Thr Gly Ile Ser Val Met Val	Ala Arg Ser Asn Gly	Thr Val Ser Pro
530	535	540
Ser Ala Phe Leu Glu Pro Tyr	Ser Pro Ala Val Trp	Val Met Met Phe
545	550	555
Val Met Cys Leu Thr Val Val	Ala Ile Thr Val Phe	Met Phe Glu Tyr
565	570	575
Phe Ser Pro Val Ser Tyr Asn	Gln Asn Leu Thr Arg	Gly Lys Thr Phe
580	585	590
Thr Ile Gly Lys Ser Val Trp	Leu Leu Trp Ala Leu	Val Phe Asn Asn
595	600	605
Ser Val Pro Ile Glu Asn Pro	Arg Gly Thr Thr Ser	Lys Ile Met Val
610	615	620
Leu Val Trp Ala Phe Phe Ala	Val Ile Phe Leu Ala	Arg Tyr Thr Ala
625	630	635
Asn Leu Ala Ala Phe Met Ile	Gln Glu Gln Tyr Ile	Asp Thr Val Ser
645	650	655
Gly Leu Ser Asp Lys Lys Phe	Gln Arg Pro Gln Asp	Gln Tyr Pro Pro
660	665	670
Phe Arg Phe Gly Thr Val Pro	Asn Gly Ser Thr Glu	Arg Asn Ile Arg
675	680	685
Ser Asn Tyr Arg Asp Met His	Thr His Met Val Lys	Phe Asn Gln Arg
690	695	700
Ser Val Glu Asp Ala Leu Thr	Ser Leu Lys Met Gly	Lys Leu Asp Ala

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705	710					715					720				
Phe Ile Tyr Asp	Ala 725	Ala	Val	Leu	Asn	Tyr 730	Met	Ala	Gly	Lys	Asp 735	Glu			
Gly Cys Lys	Leu 740	Val	Thr	Ile	Gly	Ser 745	Gly	Lys	Val	Phe	Ala 750	Thr	Thr		
Gly Tyr	Gly 755	Ile	Ala	Met	Gln	Lys 760	Asp	Ser	His	Trp	Lys 765	Arg	Ala	Ile	
Asp	Leu 770	Ala	Leu	Leu	Gln	Phè 775	Leu	Gly	Asp	Gly	Glu 780	Thr	Gln	Lys	Leu
Glu 785	Thr	Val	Trp	Leu	Ser 790	Gly	Ile	Cys	Gln	Asn 795	Glu	Lys	Asn	Glu	Val 800
Met	Ser	Ser	Lys	Leu 805	Asp	Ile	Asp	Asn	Met 810	Gly	Gly	Val	Phe	Tyr 815	Met
Leu	Leu	Val	Ala 820	Met	Gly	Leu	Ala	Leu 825	Leu	Val	Phe	Ala	Trp 830	Glu	His
Leu	Val	Tyr 835	Trp	Lys	Leu	Arg	His 840	Ser	Val	Pro	Asn	Ser 845	Ser	Gln	Leu
Asp	Phe 850	Leu	Leu	Ala	Phe	Ser 855	Arg	Gly	Ile	Tyr	Ser 860	Cys	Phe	Ser	Gly
Val 865	Gln	Ser	Leu	Ala	Ser 870	Pro	Pro	Arg	Gln	Ala 875	Ser	Pro	Asp	Leu	Thr 880
Ala	Ser	Ser	Ala	Gln 885	Ala	Ser	Val	Leu	Lys 890	Ile	Leu	Gln	Ala	Ala 895	Arg
Asp	Met	Val	Thr 900	Thr	Ala	Gly	Val	Ser 905	Asn	Ser	Leu	Asp	Arg 910	Ala	Thr
Arg	Thr	Ile 915	Glu	Asn	Trp	Gly	Gly 920	Gly	Arg	Arg	Ala	Pro 925	Pro	Pro	Ser
Pro	Cys 930	Pro	Thr	Pro	Arg	Ser 935	Gly	Pro	Ser	Pro	Cys 940	Leu	Pro	Thr	Pro
Asp 945	Pro	Pro	Pro	Glu	Pro 950	Ser	Pro	Thr	Gly	Trp 955	Gly	Pro	Pro	Asp	Gly 960
Gly	Arg	Ala	Ala	Leu 965	Val	Arg	Arg	Ala	Pro 970	Gln	Pro	Pro	Gly	Arg 975	Pro
Pro	Thr	Pro	Gly 980	Pro	Pro	Leu	Ser	Asp 985	Val	Ser	Arg	Val	Ser 990	Arg	Arg
Pro	Ala	Trp 995	Glu	Ala	Arg	Trp	Pro 1000	Val	Arg	Thr	Gly	His 1005	Cys	Gly	Arg
His	Leu 1010	Ser	Ala	Ser	Glu	Arg 1015	Pro	Leu	Ser	Pro	Ala 1020	Arg	Cys	His	Tyr
Ser 1025	Ser	Phe	Pro	Arg	Ala 1030	Asp	Arg	Ser	Gly	Arg 1035	Pro	Phe	Leu	Pro	Leu 1040
Phe	Pro	Glu	Pro	Pro 1045	Glu	Leu	Glu	Asp	Leu 1050	Pro	Leu	Leu	Gly	Pro 1055	Glu
Gln	Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	Ala	Ala	Trp	Ala	Arg	Gly

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1060	1065	1070
Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe 1075 1080 1085		
Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala 1090 1095 1100		
Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser 1105 1110 1115 1120		
Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala 1125 1130 1135		
Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His 1140 1145 1150		
Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro 1155 1160 1165		
Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly 1170 1175 1180		
His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly 1185 1190 1195 1200		
Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro 1205 1210 1215		
Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1220 1225 1230		

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4017 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 189..3848

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCCTTAATAA GATTTCGNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCGCGGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAAC TACAGCCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	

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35					40					45						
CGT Arg	GTC Val	CGC Arg	CTC Leu 50	ACC Thr	CCC Pro	CAG Gln	AGC Ser	TTC Phe 55	CTG Leu	GAC Asp	CTA Leu	CCC Pro	CTG Leu 60	GAG Glu	ATC Ile	374
CAG Gln	CCG Pro	CTC Leu 65	ACA Thr	GTT Val	GGG Gly	GTC Val	AAC Asn 70	ACC Thr	ACC Thr	AAC Asn	CCC Pro	AGC Ser 75	AGC Ser	CTC Leu	CTC Leu	422
ACC Thr	CAG Gln 80	ATC Ile	TGC Cys	GGC Gly	CTC Leu	CTG Leu 85	GGT Gly	GCT Ala	GCC Ala	CAC His	GTC Val 90	CAC His	GGC Gly	ATT Ile	GTC Val	470
TTT Phe 95	GAG Glu	GAC Asp	AAC Asn	GTG Val	GAC Asp 100	ACC Thr	GAG Glu	GCG Ala	GTG Val	GCC Ala 105	CAG Gln	ATC Ile	CTT Leu	GAC Asp	TTC Phe 110	518
ATC Ile	TCC Ser	TCC Ser	CAG Gln 115	ACC Thr	CAT His	GTG Val	CCC Pro	ATC Ile	CTC Leu 120	AGC Ser	ATC Ile	AGC Ser	GGA Gly	GGC Gly 125	TCT Ser	566
GCT Ala	GTG Val	GTC Val	CTC Leu 130	ACC Thr	CCC Pro	AAG Lys	GAG Glu	CCG Pro 135	GGC Gly	TCC Ser	GCC Ala	TTC Phe	CTG Leu 140	CAG Gln	CTG Leu	614
GGC Gly	GTG Val	TCC Ser 145	CTG Leu	GAG Glu	CAG Gln	CAG Gln	CTG Leu 150	CAG Gln	GTG Val	CTG Leu	TTC Phe	AAG Lys 155	GTG Val	CTG Leu	GAA Glu	662
GAG Glu	TAC Tyr 160	GAC Asp	TGG Trp	AGC Ser	GCC Ala	TTC Phe 165	GCC Ala	GTC Val	ATC Ile	ACC Thr	AGC Ser 170	CTG Leu	CAC His	CCG Pro	GGC Gly	710
CAC His 175	GCG Ala	CTC Leu	TTC Phe	CTG Leu	GAG Glu 180	GGC Gly	GTG Val	CGC Arg	GCC Ala	GTC Val 185	GCC Ala	GAC Asp	GCC Ala	AGC Ser	CAC His 190	758
GTG Val	AGT Ser	TGG Trp	CGG Arg 195	CTG Leu	CTG Leu	GAC Asp	GTG Val	GTC Val	ACG Thr 200	CTG Leu	GAA Glu	CTG Leu	GAC Asp	CCG Pro 205	GGA Gly	806
GGG Gly	CCG Pro	CGC Arg 210	GCG Ala	CGC Arg	ACG Thr	CAG Gln	CGC Arg	CTG Leu 215	CTG Leu	CGC Arg	CAG Gln	CTC Leu 220	GAC Asp 220	GCG Ala	CCC Pro	854
GTG Val	TTT Phe 225	GTG Val	GCC Ala	TAC Tyr	TGC Cys	TCG Ser	CGC Arg 230	GAG Glu	GAG Glu	GCC Ala	GAG Glu 235	CTC Val 235	CTC Leu	TTC Phe	GCC Ala	902
GAG Glu	GCG Ala 240	GCG Ala	CAG Gln	GCC Ala	GGT Gly	CTG Leu 245	GTG Val	GGG Gly	CCC Pro	GGC Gly	CAC His 250	GTG Val	TGG Trp	CTG Leu	GTG Val	950
CCC Pro 255	AAC Asn	CTG Leu	GCG Ala	CTG Leu	GGC Gly 260	AGC Ser	ACC Thr	GAT Asp	GCG Ala	CCC Pro 265	CCC Pro	GCC Ala	ACC Thr	TTC Phe	CCC Pro 270	998
GTG Val	GGC Gly	CTC Leu	ATC Ile	AGC Ser 275	GTC Val	GTC Val	ACC Thr	GAG Glu	AGC Ser 280	TGG Trp	CGC Arg	CTC Leu	AGC Ser	CTG Leu 285	CGC Arg	1046
CAG Gln	AAG Lys	GTG Val 290	CGC Arg	GAC Asp	GGC Gly	GTG Val	GCC Ala	ATT Ile 295	CTG Leu	GCC Ala	CTG Leu	GGC Gly 300	GCC Ala	CAC His	AGC Ser	1094
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142

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Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
		320				325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
		335			340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr		Val	Ala	Thr	Leu	Glu	Arg	Pro	Phe	Val	
		400				405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
					420				425						430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			
AAG	AAG	CTG	GCC	AGA	GTG	GTC	AAA	TTC	TCC	TAC	GAC	CTG	TAC	CTG	GTG	1622
Lys	Lys	Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	
		465					470					475				
ACC	AAC	GGC	AAG	CAT	GGC	AAG	CGG	GTG	CGC	GGC	GTA	TGG	AAC	GGC	ATG	1670
Thr	Asn	Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	
		480				485					490					
ATT	GGG	GAG	GTG	TAC	TAC	AAG	CGG	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	1718
Ile	Gly	Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	
					500					505					510	
ACC	ATC	AAT	GAG	GAA	CGC	TCC	GAG	ATC	GTA	GAC	TTC	TCT	GTA	CCC	TTT	1766
Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	
				515					520					525		
GTG	GAG	ACG	GGC	ATC	AGT	GTG	ATG	GTG	GCT	CGC	AGC	AAT	GGC	ACC	GTC	1814
Val	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	
			530				535						540			
TCC	CCC	TCG	GCC	TTC	TTG	GAG	CCA	TAT	AGC	CCT	GCA	GTG	TGG	GTG	ATG	1862
Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	
			545				550					555				
ATG	TTT	GTC	ATG	TGC	CTC	ACT	GTG	GTG	GCC	ATC	ACC	GTC	TTC	ATG	TTC	1910
Met	Phe	Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	
		560				565					570					

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GAG Glu 575	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val 580	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn 585	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys 590	1958
AAG Lys	TCC Ser	GGG Gly	GGC Gly	CCA Pro 595	GCT Ala	TTC Phe	ACT Thr	ATC Ile	GGC Gly 600	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu 605	CTG Leu	2006
TGG Trp	GCG Ala	CTG Leu	GTC Val 610	TTC Phe	AAC Asn	AAC Asn	TCA Ser	GTG Val 615	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro 620	CGG Arg	GGC Gly	2054
ACC Thr	ACC Thr	AGC Ser 625	AAG Lys	ATC Ile	ATG Met	GTT Val	CTG Leu 630	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe 635	GCT Ala	GTC Val	ATC Ile	2102
TTC Phe 640	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	ACG Thr	GCC Ala 645	AAC Asn	CTG Leu	GCC Ala	GCC Ala 650	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu	2150
CAA Gln 655	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	GTG Val 660	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp 665	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg 670	2198
CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr 675	CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe 680	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn 685	GGC Gly	2246
AGC Ser	ACG Thr	GAG Glu	CGG Arg 690	AAC Asn	ATC Ile	CGC Arg	AGT Ser	AAC Asn 695	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His 700	ACC Thr	CAC His	2294
ATG Met	GTC Val	AAG Lys 705	TTC Phe	AAC Asn	CAG Gln	CGC Arg	TCG Ser 710	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu 715	ACC Thr	AGC Ser	CTC Leu	2342
AAG Lys 720	ATG Met	GGC Gly	AAG Lys	GAC Asp	GAG Glu	GGC Gly 725	TGC Cys	AAG Lys	CTG Leu	GTC Val	ACC Thr 730	ATT Ile	GGG Gly	TCT Ser	GGC Gly	2390
AAG Lys 735	GTC Val	TTT Phe	GCT Ala	ACC Thr	ACT Thr 740	GGC Gly	TAC Tyr	GGC Gly	ATC Ile	GCC Ala 745	ATG Met	CAG Gln	AAG Lys	GAC Asp	TCC Ser 750	2438
CAC His	TGG Trp	AAG Lys	CGG Arg	GCC Ala 755	ATA Ile	GAC Asp	CTG Leu	GCG Ala	CTC Leu 760	TTG Leu	CAG Gln	TTC Phe	CTG Leu	GGG Gly 765	GAC Asp	2486
GGA Gly	GAG Glu	ACA Thr	CAG Gln 770	AAA Lys	CTG Leu	GAG Glu	ACA Thr 775	GTG Val	TGG Trp	CTC Leu	TCA Ser	GGG Gly 780	ATC Ile	TGC Cys	CAG Gln	2534
AAT Asn	GAG Glu	AAG Lys 785	AAC Asn	GAG Glu	GTG Val	ATG Met	AGC Ser 790	AGC Ser	AAG Lys	CTG Leu	GAC Asp	ATC Ile 795	GAC Asp	AAC Asn	ATG Met	2582
GGA Gly 800	GGC Gly	GTC Val	TTC Phe	TAC Tyr	ATG Met 805	CTG Leu	CTG Leu	GTG Val	GCC Ala	ATG Met	GGG Gly 810	CTG Leu	GCC Ala	CTG Leu	CTG Leu	2630
GTC Val 815	TTC Phe	GCC Ala	TGG Trp	GAG Glu	CAC His 820	CTG Leu	GTC Val	TAC Tyr	TGG Trp	AAG Lys 825	CTG Leu	CGC Arg	CAC His	TCG Ser	GTG Val 830	2678
CCC Pro	AAC Asn	TCA Ser	TCC Ser	CAG Gln 835	CTG Leu	GAC Asp	TTC Phe	CTG Leu	CTG Leu 840	GCT Ala	TTC Phe	AGC Ser	AGG Arg	GGC Gly 845	ATC Ile	2726



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TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	2774
Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	
			850					855					860			
GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	2822
Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	
		865					870					875				
ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	AAC	2870
Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	
	880					885					890					
TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	CGC	2918
Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	
	895				900				905						910	
CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	2966
Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	
				915					920					925		
CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	GGC	3014
Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	
			930					935					940			
TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	3062
Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	
		945					950					955				
CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	3110
Gln	Pro	Pro	Gly	Arg	Pro	Thr	Pro	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	
	960				965						970					
TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	CGG	3158
Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	
	975				980				985						990	
ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	TCG	3206
Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	
				995					1000					1005		
CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	CCT	CGA	GCC	GAC	CGA	TCC	GGC	3254
Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	
			1010					1015					1020			
CGC	CCC	TTC	CTC	CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG	CTG	GAG	GAC	CTG	3302
Arg	Pro	Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	
		1025				1030						1035				
CCG	CTG	CTC	GGT	CCG	GAG	CAG	CTG	GCC	CGG	CGG	GAG	GCC	CTG	CTG	AAC	3350
Pro	Leu	Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	
	1040					1045					1050					
GCG	GCC	TGG	GCC	CGG	GGC	TCG	CGC	CCG	AGT	CAC	GCT	TCC	CTG	CCC	AGC	3398
Ala	Ala	Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	Ser	Leu	Pro	Ser	
	1055				1060					1065					1070	
TCC	GTG	GCC	GAG	GCC	TTC	GCT	CGG	CCC	AGC	TCG	CTG	CCC	GCT	GGG	TGC	3446
Ser	Val	Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	Pro	Ala	Gly	Cys	
				1075					1080					1085		
ACC	GGC	CCC	GCC	TGC	GCC	CGC	CCC	GAC	GGC	CAC	TCG	GCC	TGC	AGG	CGC	3494
Thr	Gly	Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	Ala	Cys	Arg	Arg	
			1090					1095					1100			
TTG	GCG	CAG	GCG	CAG	TCG	ATG	TGC	TTG	CCG	ATC	TAC	CGG	GAG	GCC	TGC	3542
Leu	Ala	Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	Arg	Glu	Ala	Cys	
		1105					1110					1115				

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CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His 1120 1125 1130	3590
GTC TGC CTG CAC GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val 1135 1140 1145 1150	3638
TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly 1155 1160 1165	3686
GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr 1170 1175 1180	3734
GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg 1185 1190 1195	3782
GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser 1200 1205 1210	3830
CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT Leu Glu Ser Glu Val 122	3885
CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA	3945
TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT	4005
CAGCTAGCCT CA	4017

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1219 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly 1 5 10 15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val 20 25 30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val 35 40 45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro 50 55 60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln 65 70 75 80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu 85 90 95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser 100 105 110

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Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
 115 120 125  
 Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
 130 135 140  
 Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
 145 150 155 160  
 Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
 165 170 175  
 Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
 180 185 190  
 Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
 195 200 205  
 Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
 210 215 220  
 Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
 225 230 235 240  
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
 245 250 255  
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
 260 265 270  
 Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
 275 280 285  
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp  
 290 295 300  
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His  
 305 310 315 320  
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu  
 325 330 335  
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr  
 340 345 350  
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
 355 360 365  
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
 370 375 380  
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
 385 390 395 400  
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
 405 410 415  
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
 420 425 430  
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
 435 440 445  
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
 450 455 460  
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn

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465		470		475		480
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly						
		485		490		495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile						
		500		505		510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu						
		515		520		525
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro						
		530		535		540
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe						
		545		550		555
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr						
		565		570		575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser						
		580		585		590
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala						
		595		600		605
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr						
		610		615		620
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu						
		625		630		635
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr						
		645		650		655
Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln						
		660		665		670
Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr						
		675		680		685
Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val						
		690		695		700
Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met						
		705		710		715
Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val						
		725		730		735
Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp						
		740		745		750
Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu						
		755		760		765
Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu						
		770		775		780
Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly						
		785		790		795
Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe						
		805		810		815
Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn						

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820					825					830					
Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser
		835					840					845			
Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser
	850					855					860				
Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu
	865					870					875				880
Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu
				885					890					895	
Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala
			900					905					910		
Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys
		915					920					925			
Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly
	930					935					940				
Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro
	945					950					955			960	
Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg
				965					970					975	
Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly
			980					985					990		
His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala
		995					1000					1005			
Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	Asp	Arg	Ser	Gly	Arg	Pro
		1010				1015					1020				
Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	Leu	Glu	Asp	Leu	Pro	Leu
	1025					1030					1035			1040	
Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	Ala	Leu	Leu	Asn	Ala	Ala
				1045					1050					1055	
Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	Ser	Leu	Pro	Ser	Ser	Val
			1060					1065					1070		
Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	Pro	Ala	Gly	Cys	Thr	Gly
		1075					1080					1085			
Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	Ala	Cys	Arg	Arg	Leu	Ala
	1090					1095					1100				
Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	Arg	Glu	Ala	Cys	Gln	Glu
	1105					1110					1115			1120	
Gly	Glu	Gln	Ala	Gly	Ala	Pro	Ala	Trp	Gln	His	Arg	Gln	His	Val	Cys
				1125					1130					1135	
Leu	His	Ala	His	Ala	His	Leu	Pro	Leu	Cys	Trp	Gly	Ala	Val	Cys	Pro
			1140					1145					1150		
His	Leu	Pro	Pro	Cys	Asp	Ser	His	Gly	Ser	Trp	Leu	Ser	Gly	Ala	Trp
	1155						1160					1165			
Gly	Pro	Leu	Gly	His	Ser	Gly	Arg	Thr	Leu	Gly	Leu	Gly	Thr	Gly	Tyr

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1170	1175	1180
Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr		
1185	1190	1195 1200
Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu		
	1205	1210 1215
Ser Glu Val		

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4077 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 189..3908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCgcgggg GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAAct TCACAGCCCCG AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	

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GCT	GTG	GTC	CTC	ACC	CCC	AAG	GAG	CCG	GGC	TCC	GCC	TTC	CTG	CAG	CTG	614
Ala	Val	Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	
			130					135					140			
GGC	GTG	TCC	CTG	GAG	CAG	CAG	CTG	CAG	GTG	CTG	TTC	AAG	GTG	CTG	GAA	662
Gly	Val	Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	
		145					150					155				
GAG	TAC	GAC	TGG	AGC	GCC	TTC	GCC	GTC	ATC	ACC	AGC	CTG	CAC	CCG	GGC	710
Glu	Tyr	Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	
	160					165				170						
CAC	GCG	CTC	TTC	CTG	GAG	GGC	GTG	CGC	GCC	GTC	GCC	GAC	GCC	AGC	CAC	758
His	Ala	Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	
	175				180					185					190	
GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	GAC	CCG	GGA	806
Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
			195						200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
	225						230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
	240				245						250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
	255				260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
			275						280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
		290					295						300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
	335				340					345					350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
			355						360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375						380		
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				

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GAC Asp 400	AGT Ser	CGG Arg	CAC His	CTG Leu	ACG Thr	GTG Val 405	GCC Ala	ACG Thr	CTG Leu	GAA Glu 410	GAG Glu	CGG Arg	CCC Pro	TTT Phe	GTC Val	1430
ATC Ile 415	GTG Val	GAG Glu	AGC Ser	CCT Pro	GAC Asp 420	CCT Pro	GGC Gly	ACA Thr	GGA Gly 425	GGC Gly	TGT Cys	GTC Val	CCC Pro	AAC Asn	ACC Thr 430	1478
GTG Val	CCC Pro	TGC Cys	CGC Arg	AGG Arg 435	CAG Gln	AGC Ser	AAC Asn	CAC His	ACC Thr 440	TTC Phe	AGC Ser	AGC Ser	GGG Gly 445	GAC Asp 445	GTG Val	1526
GCC Ala	CCC Pro	TAC Tyr 450	ACC Thr	AAG Lys	CTC Leu	TGC Cys	TGT Cys 455	AAG Lys	GGA Gly	TTC Phe	TGC Cys	ATC Ile 460	GAC Asp 460	ATC Ile	CTC Leu	1574
AAG Lys 465	AAG Lys	CTG Leu	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys 470	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu 475	TAC Tyr	CTG Leu	GTG Val	1622
ACC Thr 480	AAC Asn	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys 485	CGG Arg	GTG Val	CGC Arg	GGC Gly	GTA Val 490	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
ATT Ile 495	GGG Gly	GAG Glu	GTG Val	TAC Tyr 500	TAC Tyr	AAG Lys	CGG Arg	GCA Ala	GAC Asp 505	ATG Met	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu 510	1718
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu 515	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val 520	GAC Asp	TTC Phe	TCT Ser	GTA Val 525	CCC Pro	TTT Phe	1766
GTG Val	GAG Glu	ACG Thr	GGC Gly 530	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val 535	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly 540	ACC Thr	GTC Val	1814
TCC Ser	CCC Pro	TCG Ser 545	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro 550	TAT Tyr	AGC Ser	CCT Pro	GCA Ala 555	GTG Val	TGG Trp	GTG Val	ATG Met	1862
ATG Met 560	TTT Phe	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr 565	GTG Val	GTG Val	GCC Ala	ATC Ile 570	ACC Thr	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
GAG Glu 575	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val 580	AGC Ser	TAC Tyr	AAC Asn	CAG Gln 585	AAC Asn	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys 590	1958
ACT Thr	TTC Phe	ACT Thr	ATC Ile	GGC Gly 595	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu 600	CTG Leu	TGG Trp	GCG Ala	CTG Leu 605	GTC Val	TTC Phe	2006
AAC Asn	AAC Asn	TCA Ser 610	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn 615	CCG Pro	CGG Arg	GGC Gly	ACC Thr	ACC Thr	AGC Ser 620	AAG Lys	ATC Ile	2054
ATG Met	GTT Val 625	CTG Leu	GTC Val	TGG Trp	GCC Ala	TTC Phe 630	TTT Phe	GCT Ala	GTC Val	ATC Ile	TTC Phe 635	CTC Leu	GCC Ala	AGA Arg	TAC Tyr	2102
ACG Thr 640	GCC Ala	AAC Asn	CTG Leu	GCC Ala	GCC Ala 645	TTC Phe	ATG Met	ATC Ile	CAA Gln	GAG Glu 650	CAA Gln	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	2150
GTG Val 655	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp 660	AAG Lys	AAG Lys	TTT Phe	CAG Gln 665	CGG Arg	CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr 670	2198



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CCA	CCT	TTC	CGC	TTC	GGC	ACG	GTG	CCC	AAC	GGC	AGC	ACG	GAG	CGG	AAC	2246
Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	
				675					680					685		
ATC	CGC	AGT	AAC	TAC	CGT	GAC	ATG	CAC	ACC	CAC	ATG	GTC	AAG	TTC	AAC	2294
Ile	Arg	Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	
			690					695					700			
CAG	CGC	TCG	GTG	GAG	GAC	GCG	CTC	ACC	AGC	CTC	AAG	ATG	GGC	TCT	GAG	2342
Gln	Arg	Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Ser	Glu	
		705					710					715				
GCT	CAG	CCT	GTC	CCC	AGG	AAG	CTG	GAT	GCC	TTC	ATC	TAT	GAT	GCT	GCT	2390
Ala	Gln	Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	
	720					725					730					
GTC	CTC	AAC	TAC	ATG	GCA	GGC	AAG	GAC	GAG	GGC	TGC	AAG	CTG	GTC	ACC	2438
Val	Leu	Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	
735					740					745					750	
ATT	GGG	TCT	GGC	AAG	GTC	TTT	GCT	ACC	ACT	GGC	TAC	GGC	ATC	GCC	ATG	2486
Ile	Gly	Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	
				755					760					765		
CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	ATA	GAC	CTG	GCG	CTC	TTG	CAG	2534
Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	
			770					775					780			
TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	AAA	CTG	GAG	ACA	GTG	TGG	CTC	TCA	2582
Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	
		785					790					795				
GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	2630
Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	
	800					805					810					
ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	ATG	CTG	CTG	GTG	GCC	ATG	GGG	2678
Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	
815					820					825					830	
CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	GAG	CAC	CTG	GTC	TAC	TGG	AAG	CTG	2726
Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	
				835					840					845		
CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	CAG	CTG	GAC	TTC	CTG	CTG	GCT	TTC	2774
Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	
			850					855					860			
AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	GGG	GTG	CAG	AGC	CTC	GCC	AGC	2822
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	
		865					870					875				
CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	CTC	ACG	GCC	AGC	TCG	GCC	CAG	GCC	2870
Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	
	880					885					890					
AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	GCC	CGC	GAC	ATG	GTG	ACC	ACG	GCG	2918
Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	
895					900				905						910	
GGC	GTA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	ACT	CGC	ACC	ATC	GAG	AAT	TGG	2966
Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	
				915					920					925		
GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	TCC	CCC	TGC	CCG	ACC	CCG	CGG	3014
Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	Ser	Pro	Cys	Pro	Thr	Pro	Arg	
			930					935					940			

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TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG	3062
Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Glu	Pro	
		945					950					955				
AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG	3110
Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val	
	960					965					970					
CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC	3158
Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro	
	975				980					985					990	
CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG	3206
Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg	
			995						1000					1005		
TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG	3254
Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu	
			1010					1015					1020			
CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	CCT	CGA	GCC	3302
Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala	
		1025					1030					1035				
GAC	CGA	TCC	GGC	CGC	CCC	TTC	CTC	CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG	3350
Asp	Arg	Ser	Gly	Arg	Pro	Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu	
	1040					1045					1050					
CTG	GAG	GAC	CTG	CCG	CTG	CTC	GGT	CCG	GAG	CAG	CTG	GCC	CGG	CGG	GAG	3398
Leu	Glu	Asp	Leu	Pro	Leu	Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu	
	1055				1060					1065					1070	
GCC	CTG	CTG	AAC	GCG	GCC	TGG	GCC	CGG	GGC	TCG	CGC	CCG	AGT	CAC	GCT	3446
Ala	Leu	Leu	Asn	Ala	Ala	Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala	
			1075						1080					1085		
TCC	CTG	CCC	AGC	TCC	GTG	GCC	GAG	GCC	TTC	GCT	CGG	CCC	AGC	TCG	CTG	3494
Ser	Leu	Pro	Ser	Ser	Val	Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu	
			1090					1095					1100			
CCC	GCT	GGG	TGC	ACC	GGC	CCC	GCC	TGC	GCC	CGC	CCC	GAC	GGC	CAC	TCG	3542
Pro	Ala	Gly	Cys	Thr	Gly	Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser	
		1105					1110					1115				
GCC	TGC	AGG	CGC	TTG	GCG	CAG	GCG	CAG	TCG	ATG	TGC	TTG	CCG	ATC	TAC	3590
Ala	Cys	Arg	Arg	Leu	Ala	Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr	
	1120					1125					1130					
CGG	GAG	GCC	TGC	CAG	GAG	GGC	GAG	CAG	GCA	GGG	GCC	CCC	GCC	TGG	CAG	3638
Arg	Glu	Ala	Cys	Gln	Glu	Gly	Glu	Gln	Ala	Gly	Ala	Pro	Ala	Trp	Gln	
	1135				1140				1145						1150	
CAC	AGA	CAG	CAC	GTC	TGC	CTG	CAC	GCC	CAC	GCC	CAC	CTG	CCA	TTG	TGC	3686
His	Arg	Gln	His	Val	Cys	Leu	His	Ala	His	Ala	His	Leu	Pro	Leu	Cys	
				1155					1160					1165		
TGG	GGG	GCT	GTC	TGT	CCT	CAC	CTT	CCA	CCC	TGT	GAC	AGC	CAC	GGC	TCC	3734
Trp	Gly	Ala	Val	Cys	Pro	His	Leu	Pro	Pro	Cys	Asp	Ser	His	Gly	Ser	
			1170					1175					1180			
TGG	CTC	TCC	GGC	GCC	TGG	GGG	CCT	CTG	GGG	CAC	AGC	GGC	AGG	ACT	CTG	3782
Trp	Leu	Ser	Gly	Ala	Trp	Gly	Pro	Leu	Gly	His	Ser	Gly	Arg	Thr	Leu	
		1185					1190					1195				
GGG	CTG	GGC	ACA	GGC	TAC	AGA	GAC	AGT	GGG	GGA	CTG	GAC	GAG	ATC	AGC	3830
Gly	Leu	Gly	Thr	Gly	Tyr	Arg	Asp	Ser	Gly	Gly	Leu	Asp	Glu	Ile	Ser	
	1200					1205					1210					

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AGT GTA GCC CGT GGC ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA      3878
Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg
1215                      1220                      1225                      1230

CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG      3925
Arg Ile Ser Ser Leu Glu Ser Glu Val
                      1235                      124

CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG      3985
CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT      4045
TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA                                4077

```

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1          5          10          15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
          20          25          30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
          35          40          45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
          50          55          60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
          65          70          75          80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
          85          90          95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
          100          105          110
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
          115          120          125
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
          130          135          140
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
          145          150          155          160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
          165          170          175
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
          180          185          190
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
          195          200          205
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
          210          215          220

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Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala	
225					230					235					240	
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn	
				245					250					255		
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	
			260					265					270			
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	
		275					280					285				
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	
	290					295					300					
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His	
305					310					315					320	
Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu	
				325					330					335		
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr	
			340					345					350			
Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	Arg	Leu	
		355					360					365				
Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	Lys	Tyr	
	370					375					380					
Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	Asp	Ser	
385					390					395					400	
Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	
				405					410					415		
Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	Val	Pro	
			420					425					430			
Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	Ala	Pro	
		435					440					445				
Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	
	450					455					460					
Leu	Ala	Arg	Val	Val	Lys	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	
465					470					475					480	
Gly	Lys	His	Gly	Lys	Arg	Val	Arg	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	
				485					490					495		
Glu	Val	Tyr	Tyr	Lys	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	
			500					505					510			
Asn	Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	
		515					520					525				
Thr	Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	
	530					535					540					
Ser	Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	
545					550					555					560	
Val	Met	Cys	Leu	Thr	Val	Val	Ala	Ile	Thr	Val	Phe	Met	Phe	Glu	Tyr	
				565					570					575		

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Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Thr	Phe
			580					585					590		
Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn
		595					600					605			
Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val
	610					615					620				
Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala
625					630					635					640
Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser
				645					650					655	
Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro
			660					665					670		
Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg
		675					680					685			
Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg
	690					695					700				
Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Ser	Glu	Ala	Gln
705					710					715					720
Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu
				725					730					735	
Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly
			740					745					750		
Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys
		755					760					765			
Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu
	770					775					780				
Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile
785					790					795					800
Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp
				805					810					815	
Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala
			820					825					830		
Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His
		835					840					845			
Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg
	850					855					860				
Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro
865					870					875					880
Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val
				885					890					895	
Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val
			900					905					910		
Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly
	915						920					925			

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Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly  
 930 935 940  
 Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Glu Pro Ser Pro  
 945 950 955 960  
 Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg  
 965 970 975  
 Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser  
 980 985 990  
 Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro  
 995 1000 1005  
 Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro  
 1010 1015 1020  
 Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg  
 1025 1030 1035 1040  
 Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu  
 1045 1050 1055  
 Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu  
 1060 1065 1070  
 Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu  
 1075 1080 1085  
 Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala  
 1090 1095 1100  
 Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys  
 1105 1110 1115 1120  
 Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu  
 1125 1130 1135  
 Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg  
 1140 1145 1150  
 Gln His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly  
 1155 1160 1165  
 Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu  
 1170 1175 1180  
 Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu  
 1185 1190 1195 1200  
 Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val  
 1205 1210 1215  
 Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile  
 1220 1225 1230  
 Ser Ser Leu Glu Ser Glu Val  
 1235

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4002 base pairs
  - (B) TYPE: nucleic acid

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(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 189..3833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	

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GTG	AGT	TGG	CGG	CTG	CTG	GAC	GTG	GTC	ACG	CTG	GAA	CTG	GAC	CCG	GGA	806
Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195					200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	854
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
			210					215					220			
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	902
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
		225					230					235				
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	950
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
	240					245					250					
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	998
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
255					260					265					270	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	1046
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275					280					285		
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	1094
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
			290					295					300			
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	1142
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
		305					310					315				
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	1190
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
	320					325					330					
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	1238
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
335					340				345						350	
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	1286
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355					360					365		
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	1334
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
			370					375					380			
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	1382
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
		385					390					395				
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	1430
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
	400					405					410					
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	1478
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
415					420				425						430	
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	1526
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435					440					445		
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	1574
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
			450					455					460			



AAG Lys	AAG Lys	CTG Leu 465	GCC Ala	AGA Arg	GTG Val	GTC Val	AAA Lys 470	TTC Phe	TCC Ser	TAC Tyr	GAC Asp	CTG Leu 475	TAC Tyr	CTG Leu	GTG Val	1622
ACC Thr	AAC Asn 480	GGC Gly	AAG Lys	CAT His	GGC Gly	AAG Lys 485	CGG Arg	GTG Val	CGC Arg	GGC Gly	GTA Val 490	TGG Trp	AAC Asn	GGC Gly	ATG Met	1670
ATT Ile 495	GGG Gly	GAG Glu	GTG Val	TAC Tyr	TAC Tyr 500	AAG Lys	CGG Arg	GCA Ala	GAC Asp	ATG Met 505	GCC Ala	ATC Ile	GGC Gly	TCC Ser	CTC Leu 510	1718
ACC Thr	ATC Ile	AAT Asn	GAG Glu	GAA Glu 515	CGC Arg	TCC Ser	GAG Glu	ATC Ile	GTA Val 520	GAC Asp	TTC Phe	TCT Ser	GTA Val	CCC Pro 525	TTT Phe	1766
GTG Val	GAG Glu	ACG Thr	GGC Gly 530	ATC Ile	AGT Ser	GTG Val	ATG Met	GTG Val 535	GCT Ala	CGC Arg	AGC Ser	AAT Asn	GGC Gly 540	ACC Thr	GTC Val	1814
TCC Ser	CCC Pro	TCG Ser 545	GCC Ala	TTC Phe	TTG Leu	GAG Glu	CCA Pro 550	TAT Tyr	AGC Ser	CCT Pro	GCA Ala	GTG Val 555	TGG Trp	GTG Val	ATG Met	1862
ATG Met	TTT Phe 560	GTC Val	ATG Met	TGC Cys	CTC Leu	ACT Thr 565	GTG Val	GTG Val	GCC Ala	ATC Ile	ACC Thr 570	GTC Val	TTC Phe	ATG Met	TTC Phe	1910
GAG Glu 575	TAC Tyr	TTC Phe	AGC Ser	CCT Pro	GTC Val 580	AGC Ser	TAC Tyr	AAC Asn	CAG Gln	AAC Asn 585	CTC Leu	ACC Thr	AGA Arg	GGC Gly	AAG Lys 590	1958
ACT Thr	TTC Phe	ACT Thr	ATC Ile	GGC Gly 595	AAG Lys	TCC Ser	GTG Val	TGG Trp	CTG Leu 600	CTG Leu	TGG Trp	GCG Ala	CTG Leu	GTC Val 605	TTC Phe	2006
AAC Asn	AAC Asn	TCA Ser 610	GTG Val	CCC Pro	ATC Ile	GAG Glu	AAC Asn	CCG Pro 615	CGG Arg	GGC Gly	ACC Thr	ACC Thr	AGC Ser 620	AAG Lys	ATC Ile	2054
ATG Met	GTT Val	CTG Leu 625	GTC Val	TGG Trp	GCC Ala	TTC Phe	TTT Phe 630	GCT Ala	GTC Val	ATC Ile	TTC Phe	CTC Leu 635	GCC Ala	AGA Arg	TAC Tyr	2102
ACG Thr	GCC Ala 640	AAC Asn	CTG Leu	GCC Ala	GCC Ala	TTC Phe 645	ATG Met	ATC Ile	CAA Gln	GAG Glu	CAA Gln 650	TAC Tyr	ATC Ile	GAC Asp	ACT Thr	2150
GTG Val 655	TCG Ser	GGC Gly	CTC Leu	AGT Ser	GAC Asp 660	AAG Lys	AAG Lys	TTT Phe	CAG Gln	CGG Arg 665	CCT Pro	CAA Gln	GAT Asp	CAG Gln	TAC Tyr 670	2198
CCA Pro	CCT Pro	TTC Phe	CGC Arg	TTC Phe 675	GGC Gly	ACG Thr	GTG Val	CCC Pro	AAC Asn 680	GGC Gly	AGC Ser	ACG Thr	GAG Glu 685	CGG Arg	AAC Asn	2246
ATC Ile	CGC Arg	AGT Ser	AAC Asn 690	TAC Tyr	CGT Arg	GAC Asp	ATG Met	CAC His 695	ACC Thr	CAC His	ATG Met	GTC Val 700	AAG Lys	TTC Phe	AAC Asn	2294
CAG Gln	CGC Arg	TCG Ser 705	GTG Val	GAG Glu	GAC Asp	GCG Ala	CTC Leu 710	ACC Thr	AGC Ser	CTC Leu	AAG Lys 715	ATG Met	GGC Gly	AAG Lys	GAC Asp	2342
GAG Glu 720	GGC Gly	TGC Cys	AAG Lys	CTG Leu	GTC Val	ACC Thr 725	ATT Ile	GGG Gly	TCT Ser	GGC Gly 730	AAG Lys	GTC Val	TTT Phe	GCT Ala	ACC Thr	2390

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ACT	GGC	TAC	GGC	ATC	GCC	ATG	CAG	AAG	GAC	TCC	CAC	TGG	AAG	CGG	GCC	2438
Thr	Gly	Tyr	Gly	Ile	Ala	Met	Gln	Lys	Asp	Ser	His	Trp	Lys	Arg	Ala	
735					740					745					750	
ATA	GAC	CTG	GCG	CTC	TTG	CAG	TTC	CTG	GGG	GAC	GGA	GAG	ACA	CAG	AAA	2486
Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Gly	Glu	Thr	Gln	Lys	
				755					760						765	
CTG	GAG	ACA	GTG	TGG	CTC	TCA	GGG	ATC	TGC	CAG	AAT	GAG	AAG	AAC	GAG	2534
Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile	Cys	Gln	Asn	Glu	Lys	Asn	Glu	
			770					775							780	
GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GGA	GGC	GTC	TTC	TAC	2582
Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Gly	Gly	Val	Phe	Tyr	
		785					790					795				
ATG	CTG	CTG	GTG	GCC	ATG	GGG	CTG	GCC	CTG	CTG	GTC	TTC	GCC	TGG	GAG	2630
Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala	Leu	Leu	Val	Phe	Ala	Trp	Glu	
	800					805					810					
CAC	CTG	GTC	TAC	TGG	AAG	CTG	CGC	CAC	TCG	GTG	CCC	AAC	TCA	TCC	CAG	2678
His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His	Ser	Val	Pro	Asn	Ser	Ser	Gln	
815					820					825					830	
CTG	GAC	TTC	CTG	CTG	GCT	TTC	AGC	AGG	GGC	ATC	TAC	AGC	TGC	TTC	AGC	2726
Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Phe	Ser	
				835					840						845	
GGG	GTG	CAG	AGC	CTC	GCC	AGC	CCA	CCG	CGG	CAG	GCC	AGC	CCG	GAC	CTC	2774
Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro	Arg	Gln	Ala	Ser	Pro	Asp	Leu	
			850					855						860		
ACG	GCC	AGC	TCG	GCC	CAG	GCC	AGC	GTG	CTC	AAG	ATT	CTG	CAG	GCA	GCC	2822
Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val	Leu	Lys	Ile	Leu	Gln	Ala	Ala	
		865					870						875			
CGC	GAC	ATG	GTG	ACC	ACG	GCG	GGC	GTA	AGC	AAC	TCC	CTG	GAC	CGC	GCC	2870
Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val	Ser	Asn	Ser	Leu	Asp	Arg	Ala	
	880					885					890					
ACT	CGC	ACC	ATC	GAG	AAT	TGG	GGT	GGC	GGC	CGC	CGT	GCG	CCC	CCA	CCG	2918
Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly	Gly	Arg	Arg	Ala	Pro	Pro	Pro	
895					900					905					910	
TCC	CCC	TGC	CCG	ACC	CCG	CGG	TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	2966
Ser	Pro	Cys	Pro	Thr	Pro	Arg	Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	
				915					920						925	
CCC	GAC	CCG	CCC	CCA	GAG	CCG	AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	3014
Pro	Asp	Pro	Pro	Pro	Glu	Pro	Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	
				930				935							940	
GGG	GGT	CGC	GCG	GCG	CTT	GTG	CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	3062
Gly	Gly	Arg	Ala	Ala	Leu	Val	Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	
		945					950					955				
CCC	CCG	ACG	CCG	GGG	CCG	CCC	CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	3110
Pro	Pro	Thr	Pro	Gly	Pro	Pro	Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	
		960				965					970					
CGC	CCA	GCC	TGG	GAG	GCG	CGG	TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	3158
Arg	Pro	Ala	Trp	Glu	Ala	Arg	Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	
				980					985						990	
AGG	CAC	CTC	TCG	GCC	TCC	GAG	CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	3206
Arg	His	Leu	Ser	Ala	Ser	Glu	Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	
				995					1000						1005	

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TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro 1010 1015 1020	3254
CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro 1025 1030 1035	3302
GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg 1040 1045 1050	3350
GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala 1055 1060 1065 1070	3398
TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys 1075 1080 1085	3446
GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln 1090 1095 1100	3494
TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln 1105 1110 1115	3542
GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala 1120 1125 1130	3590
CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro 1135 1140 1145 1150	3638
CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu 1155 1160 1165	3686
GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser 1170 1175 1180	3734
GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe 1185 1190 1195	3782
CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1200 1205 1210	3830
TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	3890 3950 4002

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1214 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Gly	Gly	Ala	Leu	Gly	Pro	Ala	Leu	Leu	Leu	Thr	Ser	Leu	Phe	Gly	1	5	10	15
Ala	Trp	Ala	Gly	Leu	Gly	Pro	Gly	Gln	Gly	Glu	Gln	Gly	Met	Thr	Val	20	25	30	
Ala	Val	Val	Phe	Ser	Ser	Ser	Gly	Pro	Pro	Gln	Ala	Gln	Phe	Arg	Val	35	40	45	
Arg	Leu	Thr	Pro	Gln	Ser	Phe	Leu	Asp	Leu	Pro	Leu	Glu	Ile	Gln	Pro	50	55	60	
Leu	Thr	Val	Gly	Val	Asn	Thr	Thr	Asn	Pro	Ser	Ser	Leu	Leu	Thr	Gln	65	70	75	80
Ile	Cys	Gly	Leu	Leu	Gly	Ala	Ala	His	Val	His	Gly	Ile	Val	Phe	Glu	85	90	95	
Asp	Asn	Val	Asp	Thr	Glu	Ala	Val	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser	100	105	110	
Ser	Gln	Thr	His	Val	Pro	Ile	Leu	Ser	Ile	Ser	Gly	Gly	Ser	Ala	Val	115	120	125	
Val	Leu	Thr	Pro	Lys	Glu	Pro	Gly	Ser	Ala	Phe	Leu	Gln	Leu	Gly	Val	130	135	140	
Ser	Leu	Glu	Gln	Gln	Leu	Gln	Val	Leu	Phe	Lys	Val	Leu	Glu	Glu	Tyr	145	150	155	160
Asp	Trp	Ser	Ala	Phe	Ala	Val	Ile	Thr	Ser	Leu	His	Pro	Gly	His	Ala	165	170	175	
Leu	Phe	Leu	Glu	Gly	Val	Arg	Ala	Val	Ala	Asp	Ala	Ser	His	Val	Ser	180	185	190	
Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	Gly	Pro	195	200	205	
Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	Val	Phe	210	215	220	
Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	Glu	Ala	225	230	235	240
Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	Pro	Asn	245	250	255	
Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	Val	Gly	260	265	270	
Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	Gln	Lys	275	280	285	
Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	Tyr	Trp	290	295	300	
Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	Val	His	305	310	315	320
Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	Leu	Leu	325	330	335	
Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	Gly	Tyr	340	345	350	

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Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
 355 360 365  
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
 370 375 380  
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
 385 390 395 400  
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
 405 410 415  
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
 420 425 430  
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
 435 440 445  
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
 450 455 460  
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn  
 465 470 475 480  
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
 485 490 495  
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
 500 505 510  
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
 515 520 525  
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
 530 535 540  
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
 545 550 555 560  
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
 565 570 575  
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Thr Phe  
 580 585 590  
 Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn  
 595 600 605  
 Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val  
 610 615 620  
 Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala  
 625 630 635 640  
 Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser  
 645 650 655  
 Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro  
 660 665 670  
 Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg  
 675 680 685  
 Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg  
 690 695 700

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Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly  
 705 710 715 720  
 Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly  
 725 730 735  
 Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp  
 740 745 750  
 Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu  
 755 760 765  
 Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met  
 770 775 780  
 Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu  
 785 790 795 800  
 Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu  
 805 810 815  
 Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp  
 820 825 830  
 Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val  
 835 840 845  
 Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala  
 850 855 860  
 Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp  
 865 870 875 880  
 Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg  
 885 890 895  
 Thr Ile Glu Asn Trp Gly Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro  
 900 905 910  
 Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp  
 915 920 925  
 Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly  
 930 935 940  
 Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro  
 945 950 955 960  
 Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro  
 965 970 975  
 Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His  
 980 985 990  
 Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser  
 995 1000 1005  
 Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe  
 1010 1015 1020  
 Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln  
 1025 1030 1035 1040  
 Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser  
 1045 1050 1055

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Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala  
 1060 1065 1070

Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg  
 1075 1080 1085

Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met  
 1090 1095 1100

Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly  
 1105 1110 1115 1120

Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala  
 1125 1130 1135

His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys  
 1140 1145 1150

Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His  
 1155 1160 1165

Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly  
 1170 1175 1180

Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly  
 1185 1190 1195 1200

Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val  
 1205 1210

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 210..4664

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGAATTTGC ATCTCTTCAA GACACAAGAT TAAAACAAAA TTTACGCTAA ATTGGATTTT 60

AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAAGAA 120

GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC 180

TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT 233  
 Met Lys Pro Arg Ala Glu Cys Cys  
 1 5

TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC 281  
 Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser  
 10 15 20

AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC 329  
 Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile  
 25 30 35 40

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CTC	GTG	GGC	ACT	TCC	GAC	GAG	GTG	GCC	ATC	AAG	GAT	GCC	CAC	GAG	AAA	377
Leu	Val	Gly	Thr	Ser	Asp	Glu	Val	Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	
			45						50					55		
GAT	GAT	TTC	CAC	CAT	CTC	TCC	GTG	GTA	CCC	CGG	GTG	GAA	CTG	GTA	GCC	425
Asp	Asp	Phe	His	His	Leu	Ser	Val	Val	Pro	Arg	Val	Glu	Leu	Val	Ala	
		60						65					70			
ATG	AAT	GAG	ACC	GAC	CCA	AAG	AGC	ATC	ATC	ACC	CGC	ATC	TGT	GAT	CTC	473
Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser	Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	
		75					80					85				
ATG	TCT	GAC	CGG	AAG	ATC	CAG	GGG	GTG	GTG	TTT	GCT	GAT	GAC	ACA	GAC	521
Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly	Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	
	90					95					100					
CAG	GAA	GCC	ATC	GCC	CAG	ATC	CTC	GAT	TTC	ATT	TCA	GCA	CAG	ACT	CTC	569
Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu	Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	
105					110					115					120	
ACC	CCG	ATC	CTG	GGC	ATC	CAC	GGG	GGC	TCC	TCT	ATG	ATA	ATG	GCA	GAT	617
Thr	Pro	Ile	Leu	Gly	Ile	His	Gly	Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	
			125						130					135		
AAG	GAT	GAA	TCC	TCC	ATG	TTC	TTC	CAG	TTT	GGC	CCA	TCA	ATT	GAA	CAG	665
Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe	Gln	Phe	Gly	Pro	Ser	Ile	Glu	Gln	
			140					145					150			
CAA	GCT	TCC	GTA	ATG	CTC	AAC	ATC	ATG	GAA	GAA	TAT	GAC	TGG	TAC	ATC	713
Gln	Ala	Ser	Val	Met	Leu	Asn	Ile	Met	Glu	Glu	Tyr	Asp	Trp	Tyr	Ile	
	155						160					165				
TTT	TCT	ATC	GTC	ACC	ACC	TAT	TTC	CCT	GGC	TAC	CAG	GAC	TTT	GTA	AAC	761
Phe	Ser	Ile	Val	Thr	Thr	Tyr	Phe	Pro	Gly	Tyr	Gln	Asp	Phe	Val	Asn	
	170					175					180					
AAG	ATC	CGC	AGC	ACC	ATT	GAG	AAT	AGC	TTT	GTG	GGC	TGG	GAG	CTA	GAG	809
Lys	Ile	Arg	Ser	Thr	Ile	Glu	Asn	Ser	Phe	Val	Gly	Trp	Glu	Leu	Glu	
185					190					195					200	
GAG	GTC	CTC	CTA	CTG	GAC	ATG	TCC	CTG	GAC	GAT	GGA	GAT	TCT	AAG	ATC	857
Glu	Val	Leu	Leu	Leu	Asp	Met	Ser	Leu	Asp	Asp	Gly	Asp	Ser	Lys	Ile	
			205						210					215		
CAG	AAT	CAG	CTC	AAG	AAA	CTT	CAA	AGC	CCC	ATC	ATT	CTT	CTT	TAC	TGT	905
Gln	Asn	Gln	Leu	Lys	Lys	Leu	Gln	Ser	Pro	Ile	Ile	Leu	Leu	Tyr	Cys	
			220					225					230			
ACC	AAG	GAA	GAA	GCC	ACC	TAC	ATC	TTT	GAA	GTG	GCC	AAC	TCA	GTA	GGG	953
Thr	Lys	Glu	Glu	Ala	Thr	Tyr	Ile	Phe	Glu	Val	Ala	Asn	Ser	Val	Gly	
		235					240					245				
CTG	ACT	GGC	TAT	GGC	TAC	ACG	TGG	ATC	GTG	CCC	AGT	CTG	GTG	GCA	GGG	1001
Leu	Thr	Gly	Tyr	Gly	Tyr	Thr	Trp	Ile	Val	Pro	Ser	Leu	Val	Ala	Gly	
	250					255					260					
GAT	ACA	GAC	ACA	GTG	CCT	GCG	GAG	TTC	CCC	ACT	GGG	CTC	ATC	TCT	GTA	1049
Asp	Thr	Asp	Thr	Val	Pro	Ala	Glu	Phe	Pro	Thr	Gly	Leu	Ile	Ser	Val	
265					270					275					280	
TCA	TAT	GAT	GAA	TGG	GAC	TAT	GGC	CTC	CCC	CCC	AGA	GTG	AGA	GAT	GGA	1097
Ser	Tyr	Asp	Glu	Trp	Asp	Tyr	Gly	Leu	Pro	Pro	Arg	Val	Arg	Asp	Gly	
			285						290					295		
ATT	GCC	ATA	ATC	ACC	ACT	GCT	GCT	TCT	GAC	ATG	CTG	TCT	GAG	CAC	AGC	1145
Ile	Ala	Ile	Ile	Thr	Thr	Ala	Ala	Ser	Asp	Met	Leu	Ser	Glu	His	Ser	
			300					305					310			



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TTC	ATC	CCT	GAG	CCC	AAA	AGC	AGT	TGT	TAC	AAC	ACC	CAC	GAG	AAG	AGA	1193
Phe	Ile	Pro	Glu	Pro	Lys	Ser	Ser	Cys	Tyr	Asn	Thr	His	Glu	Lys	Arg	
		315					320					325				
ATC	TAC	CAG	TCC	AAT	ATG	CTA	AAT	AGG	TAT	CTG	ATC	AAT	GTC	ACT	TTT	1241
Ile	Tyr	Gln	Ser	Asn	Met	Leu	Asn	Arg	Tyr	Leu	Ile	Asn	Val	Thr	Phe	
		330				335					340					
GAG	GGG	AGG	AAT	TTG	TCC	TTC	AGT	GAA	GAT	GGC	TAC	CAG	ATG	CAC	CCG	1289
Glu	Gly	Arg	Asn	Leu	Ser	Phe	Ser	Glu	Asp	Gly	Tyr	Gln	Met	His	Pro	
		345			350					355					360	
AAA	CTG	GTG	ATA	ATT	CTT	CTG	AAC	AAG	GAG	AGG	AAG	TGG	GAA	AGG	GTG	1337
Lys	Leu	Val	Ile	Ile	Leu	Leu	Asn	Lys	Glu	Arg	Lys	Trp	Glu	Arg	Val	
				365					370					375		
GGG	AAG	TGG	AAA	GAC	AAG	TCC	CTG	CAG	ATG	AAG	TAC	TAT	GTG	TGG	CCC	1385
Gly	Lys	Trp	Lys	Asp	Lys	Ser	Leu	Gln	Met	Lys	Tyr	Tyr	Val	Trp	Pro	
			380					385					390			
CGA	ATG	TGT	CCA	GAG	ACT	GAA	GAG	CAG	GAG	GAT	GAC	CAT	CTG	AGC	ATT	1433
Arg	Met	Cys	Pro	Glu	Thr	Glu	Glu	Gln	Glu	Asp	Asp	His	Leu	Ser	Ile	
		395				400						405				
GTG	ACC	CTG	GAG	GAG	GCA	CCA	TTT	GTC	ATT	GTG	GAA	AGT	GTG	GAC	CCT	1481
Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe	Val	Ile	Val	Glu	Ser	Val	Asp	Pro	
		410				415					420					
CTG	AGT	GGA	ACC	TGC	ATG	AGG	AAC	ACA	GTC	CCC	TGC	CAA	AAA	CGC	ATA	1529
Leu	Ser	Gly	Thr	Cys	Met	Arg	Asn	Thr	Val	Pro	Cys	Gln	Lys	Arg	Ile	
		425			430					435					440	
GTC	ACT	GAG	AAT	AAA	ACA	GAC	GAG	GAG	CCG	GGT	TAC	ATC	AAA	AAA	TGC	1577
Val	Thr	Glu	Asn	Lys	Thr	Asp	Glu	Glu	Pro	Gly	Tyr	Ile	Lys	Lys	Cys	
				445					450					455		
TGC	AAG	GGG	TTC	TGT	ATT	GAC	ATC	CTT	AAG	AAA	ATT	TCT	AAA	TCT	GTG	1625
Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Lys	Ile	Ser	Lys	Ser	Val	
			460					465					470			
AAG	TTC	ACC	TAT	GAC	CTT	TAC	CTG	GTT	ACC	AAT	GGC	AAG	CAT	GGG	AAG	1673
Lys	Phe	Thr	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	Lys	His	Gly	Lys	
		475					480					485				
AAA	ATC	AAT	GGA	ACC	TGG	AAT	GGT	ATG	ATT	GGA	GAG	GTG	GTC	ATG	AAG	1721
Lys	Ile	Asn	Gly	Thr	Trp	Asn	Gly	Met	Ile	Gly	Glu	Val	Val	Met	Lys	
		490				495					500					
AGG	GCC	TAC	ATG	GCA	GTG	GGC	TCA	CTC	ACC	ATC	AAT	GAG	GAA	CGA	TCG	1769
Arg	Ala	Tyr	Met	Ala	Val	Gly	Ser	Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	
		505			510					515					520	
GAG	GTG	GTC	GAC	TTC	TCT	GTG	CCC	TTC	ATA	GAG	ACA	GGC	ATC	AGT	GTC	1817
Glu	Val	Val	Asp	Phe	Ser	Val	Pro	Phe	Ile	Glu	Thr	Gly	Ile	Ser	Val	
				525					530					535		
ATG	GTG	TCA	CGC	AGC	AAT	GGG	ACT	GTC	TCA	CCT	TCT	GCC	TTC	TTA	GAG	1865
Met	Val	Ser	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	
				540				545					550			
CCA	TTC	AGC	GCT	GAC	GTA	TGG	GTG	ATG	ATG	TTT	GTG	ATG	CTG	CTC	ATC	1913
Pro	Phe	Ser	Ala	Asp	Val	Trp	Val	Met	Met	Phe	Val	Met	Leu	Leu	Ile	
		555					560					565				
GTC	TCA	GCC	GTG	GCT	GTC	TTT	GTC	TTT	GAG	TAC	TTC	AGC	CCT	GTG	GGT	1961
Val	Ser	Ala	Val	Ala	Val	Phe	Val	Phe	Glu	Tyr	Phe	Ser	Pro	Val	Gly	
		570				575					580					

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TAT Tyr 585	AAC Asn	AGG Arg	TGC Cys	CTC Leu	GCT Ala 590	GAT Asp	GGC Gly	AGA Arg	GAG Glu 595	CCT Pro	GGT Gly	GGA Gly	CCC Pro	TCT Ser	TTC Phe 600	2009
ACC Thr	ATC Ile	GGC Gly	AAA Lys	GCT Ala 605	ATT Ile	TGG Trp	TTG Leu	CTC Leu	TGG Trp 610	GGT Gly	CTG Leu	GTG Val	TTT Phe 615	AAC Asn	AAC Asn	2057
TCC Ser	GTA Val	CCT Pro	GTG Val 620	CAG Gln	AAC Asn	CCA Pro	AAG Lys	GGG Gly 625	ACC Thr	ACC Thr	TCC Ser	AAG Lys	ATC Ile 630	ATG Met	GTG Val	2105
TCA Ser	GTG Val	TGG Trp 635	GCC Ala	TTC Phe	TTT Phe	GCT Ala	GTC Val 640	ATC Ile	TTC Phe	CTG Leu	GCC Ala	AGC Ser 645	TAC Tyr	ACT Thr	GCC Ala	2153
AAC Asn 650	TTA Leu	GCT Ala	GCC Ala	TTC Phe	ATG Met	ATC Ile 655	CAA Gln	GAG Glu	GAA Glu	TAT Tyr	GTG Val 660	GAC Asp	CAG Gln	GTT Val	TCT Ser	2201
GGC Gly 665	CTG Leu	AGC Ser	GAC Asp	AAA Lys 670	AAG Lys	TTC Phe	CAG Gln	AGA Arg	CCT Pro	AAT Asn 675	GAC Asp	TTC Phe	TCA Ser	CCC Pro	CCT Pro 680	2249
TTC Phe	CGC Arg	TTT Phe	GGG Gly	ACC Thr 685	GTG Val	CCC Pro	AAC Asn	GGC Gly	AGC Ser 690	ACA Thr	GAG Glu	AGA Arg	AAT Asn	ATT Ile 695	CGC Arg	2297
AAT Asn	AAC Asn	TAT Tyr 700	GCA Ala	GAA Glu	ATG Met	CAT His	GCC Ala	TAC Tyr 705	ATG Met	GGA Gly	AAG Lys	TTC Phe 710	AAC Asn	CAG Gln	AGG Arg	2345
GGT Gly	GTA Val 715	GAT Asp	GAT Asp	GCA Ala	TTG Leu	CTC Leu	TCC Ser 720	CTG Leu	AAA Lys	ACA Thr	GGG Gly 725	AAA Lys	CTG Leu	GAT Asp	GCC Ala	2393
TTC Phe 730	ATC Ile	TAT Tyr	GAT Asp	GCA Ala	GCA Ala	GTG Val 735	CTG Leu	AAC Asn	TAT Tyr	ATG Met	GCA Ala 740	GGC Gly	AGA Arg	GAT Asp	GAA Glu	2441
GGC Gly 745	TGC Cys	AAG Lys	CTG Leu	GTG Val 750	ACC Thr	ATT Ile	GGC Gly	AGT Ser	GGG Gly 755	AAG Lys	GTC Val	TTT Phe	GCT Ala	TCC Ser	ACT Thr 760	2489
GGC Gly	TAT Tyr	GGC Gly	ATT Ile	GCC Ala 765	ATC Ile	CAA Gln	AAA Lys	GAT Asp 770	TCT Ser	GGG Gly	TGG Trp	AAG Lys	CGC Arg	CAG Gln 775	GTG Val	2537
GAC Asp	CTT Leu	GCT Ala 780	ATC Ile	CTG Leu	CAG Gln	CTC Leu	TTT Phe 785	GGA Gly 785	GAT Asp	GGG Gly	GAG Glu	ATG Met	GAA Glu 790	GAA Glu	CTG Leu	2585
GAA Glu	GCT Ala 795	CTC Leu	TGG Trp	CTC Leu	ACT Thr	GGC Gly	ATT Ile 800	TGT Cys	CAC His	AAT Asn	GAG Glu	AAG Lys 805	AAT Asn	GAG Glu	GTC Val	2633
ATG Met 810	AGC Ser	AGC Ser	CAG Gln	CTG Leu	GAC Asp	ATT Ile 815	GAC Asp	AAC Asn	ATG Met	GCA Ala	GGG Gly 820	GTC Val	TTC Phe	TAC Tyr	ATG Met	2681
TTG Leu 825	GGG Gly	GCG Ala	GCC Ala	ATG Met	GCT Ala 830	CTC Leu	AGC Ser	CTC Leu	ATC Ile	ACC Thr 835	TTC Phe	ATC Ile	TGC Cys	GAA Glu	CAC His 840	2729
CTT Leu	TTC Phe	TAT Tyr	TGG Trp	CAG Gln 845	TTC Phe	CGA Arg	CAT His	TGC Cys	TTT Phe 850	ATG Met	GGT Gly	GTC Val	TGT Cys	TCT Ser	GGC Gly 855	2777

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AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC	2825
Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile	
860 865 870	
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC	2873
His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr	
875 880 885	
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG	2921
Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr	
890 895 900	
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC	2969
Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser	
905 910 915 920	
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG	3017
Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu	
925 930 935	
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG	3065
His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro	
940 945 950	
CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA	3113
Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg	
955 960 965	
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC	3161
Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His	
970 975 980	
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC	3209
Tyr His His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile	
985 990 995 1000	
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG	3257
Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg	
1005 1010 1015	
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC	3305
Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His	
1020 1025 1030	
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC	3353
Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg	
1035 1040 1045	
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA	3401
Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser	
1050 1055 1060	
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG	3449
Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg	
1065 1070 1075 1080	
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC	3497
Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala	
1085 1090 1095	
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA	3545
Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg	
1100 1105 1110	
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG	3593
Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly	
1115 1120 1125	

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CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881
TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gln Glu Leu Asp Gln Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409

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AGC AAA TCC TAC TTC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val 148	4701
TAAGGCTGTG GGTGCGGTGA TGC GCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGTTCC	4761
CATTTGCTCC TTTCTTGTTT TAATTTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG	4821
GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTTCA CAGTTCTCTC CTTCTTCCCC	4881
CCGCTGTGAG CCATTCCTGT TCCCATGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG	4941
GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCCTCC TGGTGTGGAA GAGCTCCTTG	5001
ATATCCTCTT TGAGTGAAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC	5061
TTTTCCCAAA CTGATCTTTT CATTTAGGTG AGGAAGCAAA AGCATCTATG TGAGACCATT	5121
TAGCACACTG CTTGTGAAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT	5181
CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTTA TATATAAGCC	5241
CAAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC	5301
ATTGGTGGCA GAGTGGATTG TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG	5361
TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTTCATGCA CACTTGACAC	5421
CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT	5481
CTTCAAGACA CAAGATTAAA ACAAATTTA CGCTAAATTG GATTTTAAAT TATCTTC	5538

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1484 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Lys	Pro	Arg	Ala	Glu	Cys	Cys	Ser	Pro	Lys	Phe	Trp	Leu	Val	Leu
1				5					10					15	

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Ala Val Leu Ala Val Ser Gly Ser Arg Ala Arg Ser Gln Lys Ser Pro  
                   20                                  25                                  30  
 Pro Ser Ile Gly Ile Ala Val Ile Leu Val Gly Thr Ser Asp Glu Val  
                   35                                  40                                  45  
 Ala Ile Lys Asp Ala His Glu Lys Asp Asp Phe His His Leu Ser Val  
                   50                                  55                                  60  
 Val Pro Arg Val Glu Leu Val Ala Met Asn Glu Thr Asp Pro Lys Ser  
                   65                                  70                                  75                                  80  
 Ile Ile Thr Arg Ile Cys Asp Leu Met Ser Asp Arg Lys Ile Gln Gly  
                                   85                                  90                                  95  
 Val Val Phe Ala Asp Asp Thr Asp Gln Glu Ala Ile Ala Gln Ile Leu  
                                   100                                  105                                  110  
 Asp Phe Ile Ser Ala Gln Thr Leu Thr Pro Ile Leu Gly Ile His Gly  
                                   115                                  120                                  125  
 Gly Ser Ser Met Ile Met Ala Asp Lys Asp Glu Ser Ser Met Phe Phe  
                                   130                                  135                                  140  
 Gln Phe Gly Pro Ser Ile Glu Gln Gln Ala Ser Val Met Leu Asn Ile  
                                   145                                  150                                  155                                  160  
 Met Glu Glu Tyr Asp Trp Tyr Ile Phe Ser Ile Val Thr Thr Tyr Phe  
                                   165                                  170                                  175  
 Pro Gly Tyr Gln Asp Phe Val Asn Lys Ile Arg Ser Thr Ile Glu Asn  
                                   180                                  185                                  190  
 Ser Phe Val Gly Trp Glu Leu Glu Glu Val Leu Leu Leu Asp Met Ser  
                                   195                                  200                                  205  
 Leu Asp Asp Gly Asp Ser Lys Ile Gln Asn Gln Leu Lys Lys Leu Gln  
                                   210                                  215                                  220  
 Ser Pro Ile Ile Leu Leu Tyr Cys Thr Lys Glu Glu Ala Thr Tyr Ile  
                                   225                                  230                                  235                                  240  
 Phe Glu Val Ala Asn Ser Val Gly Leu Thr Gly Tyr Gly Tyr Thr Trp  
                                   245                                  250                                  255  
 Ile Val Pro Ser Leu Val Ala Gly Asp Thr Asp Thr Val Pro Ala Glu  
                                   260                                  265                                  270  
 Phe Pro Thr Gly Leu Ile Ser Val Ser Tyr Asp Glu Trp Asp Tyr Gly  
                                   275                                  280                                  285  
 Leu Pro Pro Arg Val Arg Asp Gly Ile Ala Ile Ile Thr Thr Ala Ala  
                                   290                                  295                                  300  
 Ser Asp Met Leu Ser Glu His Ser Phe Ile Pro Glu Pro Lys Ser Ser  
                                   305                                  310                                  315                                  320  
 Cys Tyr Asn Thr His Glu Lys Arg Ile Tyr Gln Ser Asn Met Leu Asn  
                                   325                                  330                                  335  
 Arg Tyr Leu Ile Asn Val Thr Phe Glu Gly Arg Asn Leu Ser Phe Ser  
                                   340                                  345                                  350  
 Glu Asp Gly Tyr Gln Met His Pro Lys Leu Val Ile Ile Leu Leu Asn  
                                   355                                  360                                  365  
 Lys Glu Arg Lys Trp Glu Arg Val Gly Lys Trp Lys Asp Lys Ser Leu

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370					375					380					
Gln 385	Met	Lys	Tyr	Tyr	Val 390	Trp	Pro	Arg	Met	Cys 395	Pro	Glu	Thr	Glu	Glu 400
Gln	Glu	Asp	Asp	His 405	Leu	Ser	Ile	Val	Thr 410	Leu	Glu	Glu	Ala	Pro	Phe 415
Val	Ile	Val	Glu 420	Ser	Val	Asp	Pro	Leu 425	Ser	Gly	Thr	Cys	Met 430	Arg	Asn
Thr	Val	Pro 435	Cys	Gln	Lys	Arg	Ile 440	Val	Thr	Glu	Asn	Lys 445	Thr	Asp	Glu
Glu	Pro 450	Gly	Tyr	Ile	Lys	Lys 455	Cys	Cys	Lys	Gly	Phe 460	Cys	Ile	Asp	Ile
Leu 465	Lys	Lys	Ile	Ser	Lys 470	Ser	Val	Lys	Phe	Thr 475	Tyr	Asp	Leu	Tyr	Leu 480
Val	Thr	Asn	Gly	Lys 485	His	Gly	Lys	Lys 490	Ile	Asn	Gly	Thr	Trp	Asn	Gly 495
Met	Ile	Gly	Glu 500	Val	Val	Met	Lys	Arg 505	Ala	Tyr	Met	Ala	Val 510	Gly	Ser
Leu	Thr	Ile 515	Asn	Glu	Glu	Arg	Ser 520	Glu	Val	Val	Asp	Phe 525	Ser	Val	Pro
Phe 530	Ile	Glu	Thr	Gly	Ile	Ser 535	Val	Met	Val	Ser	Arg 540	Ser	Asn	Gly	Thr
Val 545	Ser	Pro	Ser	Ala	Phe 550	Leu	Glu	Pro	Phe	Ser 555	Ala	Asp	Val	Trp	Val 560
Met	Met	Phe	Val	Met 565	Leu	Leu	Ile	Val	Ser 570	Ala	Val	Ala	Val	Phe	Val 575
Phe	Glu	Tyr	Phe 580	Ser	Pro	Val	Gly	Tyr 585	Asn	Arg	Cys	Leu	Ala 590	Asp	Gly
Arg	Glu	Pro 595	Gly	Gly	Pro	Ser	Phe 600	Thr	Ile	Gly	Lys	Ala 605	Ile	Trp	Leu
Leu 610	Trp	Gly	Leu	Val	Phe	Asn 615	Asn	Ser	Val	Pro	Val 620	Gln	Asn	Pro	Lys
Gly 625	Thr	Thr	Ser	Lys	Ile 630	Met	Val	Ser	Val	Trp 635	Ala	Phe	Phe	Ala	Val 640
Ile	Phe	Leu	Ala	Ser 645	Tyr	Thr	Ala	Asn	Leu 650	Ala	Ala	Phe	Met	Ile	Gln 655
Glu	Glu	Tyr	Val 660	Asp	Gln	Val	Ser	Gly 665	Leu	Ser	Asp	Lys	Lys 670	Phe	Gln
Arg	Pro	Asn 675	Asp	Phe	Ser	Pro	Pro 680	Phe	Arg	Phe	Gly	Thr 685	Val	Pro	Asn
Gly 690	Ser	Thr	Glu	Arg	Asn	Ile 695	Arg	Asn	Asn	Tyr	Ala 700	Glu	Met	His	Ala
Tyr 705	Met	Gly	Lys	Phe	Asn 710	Gln	Arg	Gly	Val	Asp 715	Asp	Ala	Leu	Leu	Ser 720
Leu	Lys	Thr	Gly	Lys 725	Leu	Asp	Ala	Phe	Ile 730	Tyr	Asp	Ala	Ala	Val	Leu 735

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Asn	Tyr	Met	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	
			740					745					750			
Ser	Gly	Lys	Val	Phe	Ala	Ser	Thr	Gly	Tyr	Gly	Ile	Ala	Ile	Gln	Lys	
		755					760					765				
Asp	Ser	Gly	Trp	Lys	Arg	Gln	Val	Asp	Leu	Ala	Ile	Leu	Gln	Leu	Phe	
	770					775					780					
Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Ala	Leu	Trp	Leu	Thr	Gly	Ile	
785					790					795					800	
Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	Ile	Asp	
			805						810					815		
Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Gly	Ala	Ala	Met	Ala	Leu	Ser	
			820					825					830			
Leu	Ile	Thr	Phe	Ile	Cys	Glu	His	Leu	Phe	Tyr	Trp	Gln	Phe	Arg	His	
		835					840					845				
Cys	Phe	Met	Gly	Val	Cys	Ser	Gly	Lys	Pro	Gly	Met	Val	Phe	Ser	Ile	
	850					855					860					
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	Ala	Ile	Glu	Glu	Arg	
865					870					875					880	
Gln	Ser	Val	Met	Asn	Ser	Pro	Thr	Ala	Thr	Met	Asn	Asn	Thr	His	Ser	
				885					890					895		
Asn	Ile	Leu	Arg	Leu	Leu	Arg	Thr	Ala	Lys	Asn	Met	Ala	Asn	Leu	Ser	
			900					905					910			
Gly	Val	Asn	Gly	Ser	Pro	Gln	Ser	Ala	Leu	Asp	Phe	Ile	Arg	Arg	Glu	
		915					920					925				
Ser	Ser	Val	Tyr	Asp	Ile	Ser	Glu	His	Arg	Arg	Ser	Phe	Thr	His	Ser	
	930					935					940					
Asp	Cys	Lys	Ser	Tyr	Asn	Asn	Pro	Pro	Cys	Glu	Glu	Asn	Leu	Phe	Ser	
945					950					955					960	
Asp	Tyr	Ile	Ser	Glu	Val	Glu	Arg	Thr	Phe	Gly	Asn	Leu	Gln	Leu	Lys	
				965					970					975		
Asp	Ser	Asn	Val	Tyr	Gln	Asp	His	Tyr	His	His	His	His	Arg	Pro	His	
			980					985					990			
Ser	Ile	Gly	Ser	Ala	Ser	Ser	Ile	Asp	Gly	Leu	Tyr	Asp	Cys	Asp	Asn	
		995					1000					1005				
Pro	Pro	Phe	Thr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Lys	Lys	Pro	Leu	Asp	
	1010					1015					1020					
Ile	Gly	Leu	Pro	Ser	Ser	Lys	His	Ser	Gln	Leu	Ser	Asp	Leu	Tyr	Gly	
1025					1030					1035					1040	
Lys	Phe	Ser	Phe	Lys	Ser	Asp	Arg	Tyr	Ser	Gly	His	Asp	Asp	Leu	Ile	
				1045					1050					1055		
Arg	Ser	Asp	Val	Ser	Asp	Ile	Ser	Thr	His	Thr	Val	Thr	Tyr	Gly	Asn	
			1060					1065					1070			
Ile	Glu	Gly	Asn	Ala	Ala	Lys	Arg	Arg	Lys	Gln	Gln	Tyr	Lys	Asp	Ser	
		1075					1080					1085				
Leu	Lys	Lys	Arg	Pro	Ala	Ser	Ala	Lys	Ser	Arg	Arg	Glu	Phe	Asp	Glu	



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1090	1095	1100
Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys 1105 1110 1115 1120		
Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln 1125 1130 1135		
Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr 1140 1145 1150		
Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser 1155 1160 1165		
Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly 1170 1175 1180		
Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn 1185 1190 1195 1200		
Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg 1205 1210 1215		
Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln 1220 1225 1230		
Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala 1235 1240 1245		
Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp 1250 1255 1260		
Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys 1265 1270 1275 1280		
Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn 1285 1290 1295		
Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys 1300 1305 1310		
Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly 1315 1320 1325		
Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala 1330 1335 1340		
Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly 1345 1350 1355 1360		
His His His His Asn Asn Pro Gly Gly Gly Tyr Met Leu Ser Lys Ser 1365 1370 1375		
Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly 1380 1385 1390		
Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln 1395 1400 1405		
Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu 1410 1415 1420		
Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala 1425 1430 1435 1440		
Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val 1445 1450 1455		

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Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His  
 1460 1465 1470

Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val  
 1475 1480

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4695 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both  
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 485..4495

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGAGAACACA GCGAGTGTGT GAGTCCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG 60

CCGCCACCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT 120

GTTGCCTGGG TAGGTCGGCC CGGCCCCCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCCCGA 180

GAAACATGTG TGGCCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA 240

GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG 300

TCCCGGCTTG CCGTTGTGCG CACCACCACT GCCGCCGCC CGGGGCCTGC CCCCACATC 360

GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTTGCC 420

CCCCCGCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCCGCA 480

GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG 529  
 Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys  
 1 5 10 15

ATG CTG CTG CTG CTG GCG CTG GCC TGC GCC AGC CCG TTC CCG GAG GAG 577  
 Met Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu  
 20 25 30

GCG CCG GGG CCG GGC GGG GCC GGT GGG CCC GGC GGC GGC CTC GGC GGG 625  
 Ala Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly  
 35 40 45

GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG 673  
 Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala  
 50 55 60

GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC 721  
 Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser  
 65 70 75

CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC 769  
 Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp  
 80 85 90 95

CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC 817  
 Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg

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				100				105				110							
GTG Val	CAC His	GGC Gly	GTG Val 115	GTC Val	TTC Phe	GAA Glu	GAC Asp	GAC Asp 120	TCG Ser	CGC Arg	GCG Ala	CCC Pro	GCC Ala 125	GTC Val	GCG Ala	865			
CCC Pro	ATC Ile	CTC Leu 130	GAC Asp	TTC Phe	CTG Leu	TCG Ser	GCG Ala 135	CAG Gln	ACC Thr	TCG Ser	CTC Leu	CCC Pro 140	ATC Ile	GTG Val	TCC Ser	913			
GAG Glu	CAC His 145	GGC Gly	GGC Gly	GCC Ala	GCG Ala	CTC Leu 150	GTG Val	CTC Leu	ACG Thr	CCC Pro	AAG Lys 155	GAG Glu	AAG Lys	GGC Gly	TCC Ser	961			
ACC Thr 160	TTC Phe	CTC Leu	CAC His	CTG Leu	GGC Gly 165	TCT Ser	TCC Ser	CCC Pro	GAG Glu	CAA Gln 170	CAG Gln	CTT Leu	CAG Gln	GTC Val	ATC Ile 175	1009			
TTT Phe	GAG Glu	GTG Val	CTG Leu	GAG Glu 180	GAG Glu	TAT Tyr	GAC Asp	TGG Trp 185	ACG Thr	TCC Ser	TTT Phe	GTA Val	GCC Ala	GTG Val 190	ACC Thr	1057			
ACT Thr	CGT Arg	GCC Ala	CCT Pro 195	GGC Gly	CAC His	CGG Arg	GCC Ala	TTC Phe 200	CTG Leu	TCC Ser	TAC Tyr	ATT Ile	GAG Glu 205	GTG Val	CTG Leu	1105			
ACT Thr	GAC Asp	GGC Gly 210	AGT Ser	CTG Leu	GTG Val	GGC Gly 215	TGG Trp	GAG Glu	CAC His	CGC Arg	GGA Gly	GCG Ala 220	CTG Leu	ACG Thr	CTG Leu	1153			
GAC Asp	CCT Pro 225	GGG Gly	GCG Ala	GGC Gly	GAG Glu	GCC Ala 230	GTG Val	CTC Leu	AGT Ser	GCC Ala	CAG Gln 235	CTC Leu	CGC Arg	AGT Ser	GTC Val	1201			
AGC Ser 240	GCG Ala	CAG Gln	ATC Ile	CGC Arg	CTG Leu 245	CTC Leu	TTC Phe	TGC Cys	GCC Ala	CGA Arg 250	GAG Glu	GAG Glu	GCC Ala	GAG Glu	CCC Pro 255	1249			
GTG Val	TTC Phe	CGC Arg	GCA Ala	GCT Ala 260	GAG Glu	GAG Glu	GCT Ala	GGC Gly 265	CTC Leu	ACT Thr	GGA Gly	TCT Ser	GGC Gly	TAC Tyr 270	GTC Val	1297			
TGG Trp	TTC Phe	ATG Met 275	GTG Val	GGG Gly	CCC Pro	CAG Gln	CTG Leu	GCT Ala 280	GGA Gly	GGC Gly	GGG Gly	GGC Gly	TCT Ser 285	GGG Gly	GCC Ala	1345			
CCT Pro	GGT Gly 290	GAG Glu	CCC Pro	CCT Pro	CTT Leu	CTG Leu	CCA Pro 295	GGA Gly	GGC Gly	GCC Ala	CCC Pro	CTG Leu 300	CCT Pro	GCC Ala	GGG Gly	1393			
CTG Leu	TTT Phe 305	GCA Ala	GTG Val	CGC Arg	TCG Ser	GCT Ala 310	GGC Gly	TGG Trp	CGG Arg	GAT Asp	GAC Asp 315	CTG Leu	GCT Ala	CGG Arg	CGA Arg	1441			
GTG Val 320	GCA Ala	GCT Ala	GGC Gly	GTG Val	GCC Ala 325	GTA Val	GTG Val	GCC Ala	AGA Arg	GGT Gly 330	GCC Ala	CAG Gln	GCC Ala	CTG Leu	CTG Leu 335	1489			
CGT Arg	GAT Asp	TAT Tyr	GGT Gly 340	TTC Phe	CTT Leu	CCT Pro	GAG Glu	CTC Leu	GGC Gly 345	CAC His	GAC Asp	TGT Cys	CGC Arg	GCC Ala 350	CAG Gln	1537			
AAC Asn	CGC Arg	ACC Thr 355	CAC His	CGC Arg	GGG Gly	GAG Glu	AGT Ser	CTG Leu 360	CAT His	AGG Arg	TAC Tyr	TTC Phe	ATG Met 365	AAC Asn	ATC Ile	1585			
ACG	TGG	GAT	AAC	CGG	GAT	TAC	TCC	TTC	AAT	GAG	GAC	GGC	TTC	CTA	GTG	1633			

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Thr	Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	
		370					375					380				
AAC	CCC	TCC	CTG	GTG	GTC	ATC	TCC	CTC	ACC	AGA	GAC	AGG	ACG	TGG	GAG	1681
Asn	Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	
	385					390					395					
GTG	GTG	GGC	AGC	TGG	GAG	CAG	CAG	ACG	CTC	CGC	CTC	AAG	TAC	CCG	CTG	1729
Val	Val	Gly	Ser	Trp	Glu	Gln	Gln	Thr	Leu	Arg	Leu	Lys	Tyr	Pro	Leu	
400					405					410					415	
TGG	TCC	CGC	TAT	GGT	CGC	TTC	CTG	CAG	CCA	GTG	GAC	GAC	ACG	CAG	CAC	1777
Trp	Ser	Arg	Tyr	Gly	Arg	Phe	Leu	Gln	Pro	Val	Asp	Asp	Thr	Gln	His	
				420					425					430		
CTC	GCG	GTG	GCC	ACG	CTG	GAG	GAA	AGG	CCG	TTT	GTC	ATC	GTG	GAG	CCT	1825
Leu	Ala	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	Ile	Val	Glu	Pro	
			435					440					445			
GCA	GAC	CCT	ATC	AGC	GGC	ACC	TGC	ATC	CGA	GAC	TCC	GTC	CCC	TGC	CGG	1873
Ala	Asp	Pro	Ile	Ser	Gly	Thr	Cys	Ile	Arg	Asp	Ser	Val	Pro	Cys	Arg	
		450					455					460				
AGC	CAG	CTC	AAC	CGA	ACC	CAC	AGC	CCT	CCA	CCG	GAT	GCC	CCC	CGC	CCG	1921
Ser	Gln	Leu	Asn	Arg	Thr	His	Ser	Pro	Pro	Pro	Asp	Ala	Pro	Arg	Pro	
	465					470					475					
GAA	AAG	CGC	TGC	TGC	AAG	GGT	TTC	TGC	ATC	GAC	ATT	CTG	AAG	CGG	CTG	1969
Glu	Lys	Arg	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	Lys	Arg	Leu	
480					485					490					495	
GCG	CAT	ACC	ATC	GGC	TTC	AGC	TAC	GAC	CTC	TAC	CTG	GTC	ACC	AAT	GGC	2017
Ala	His	Thr	Ile	Gly	Phe	Ser	Tyr	Asp	Leu	Tyr	Leu	Val	Thr	Asn	Gly	
				500					505					510		
AAG	CAC	GGA	AAG	AAG	ATC	GAT	GGC	GTC	TGG	AAC	GGC	ATG	ATC	GGG	GAG	2065
Lys	His	Gly	Lys	Lys	Ile	Asp	Gly	Val	Trp	Asn	Gly	Met	Ile	Gly	Glu	
			515					520					525			
GTG	TTC	TAC	CAG	CGC	GCA	GAC	ATG	GCC	ATC	GGC	TCC	CTC	ACC	ATC	AAC	2113
Val	Phe	Tyr	Gln	Arg	Ala	Asp	Met	Ala	Ile	Gly	Ser	Leu	Thr	Ile	Asn	
		530					535					540				
GAG	GAG	CGC	TCC	GAG	ATC	GTG	GAC	TTC	TCC	GTC	CCC	TTC	GTG	GAG	ACC	2161
Glu	Glu	Arg	Ser	Glu	Ile	Val	Asp	Phe	Ser	Val	Pro	Phe	Val	Glu	Thr	
	545					550					555					
GGC	ATC	AGC	GTC	ATG	GTG	GCG	CGC	AGC	AAT	GGC	ACG	GTG	TCC	CCC	TCG	2209
Gly	Ile	Ser	Val	Met	Val	Ala	Arg	Ser	Asn	Gly	Thr	Val	Ser	Pro	Ser	
560					565					570					575	
GCC	TTC	CTC	GAG	CCC	TAC	AGC	CCC	GCC	GTG	TGG	GTG	ATG	ATG	TTC	GTC	2257
Ala	Phe	Leu	Glu	Pro	Tyr	Ser	Pro	Ala	Val	Trp	Val	Met	Met	Phe	Val	
				580					585					590		
ATG	TGC	CTC	ACT	GTG	GTC	GCC	GTC	ACT	GTT	TTC	ATC	TTC	GAG	TAC	CTC	2305
Met	Cys	Leu	Thr	Val	Val	Ala	Val	Thr	Val	Phe	Ile	Phe	Glu	Tyr	Leu	
				595				600					605			
AGT	CCT	GTT	GGT	TAC	AAC	CGC	AGC	CTG	GCC	ACG	GGC	AAG	CGC	CCT	GGC	2353
Ser	Pro	Val	Gly	Tyr	Asn	Arg	Ser	Leu	Ala	Thr	Gly	Lys	Arg	Pro	Gly	
		610					615					620				
GGT	TCA	ACC	TTC	ACC	ATT	GGG	AAA	TCC	ATC	TGG	CTG	CTC	TGG	GCC	CTG	2401
Gly	Ser	Thr	Phe	Thr	Ile	Gly	Lys	Ser	Ile	Trp	Leu	Leu	Trp	Ala	Leu	
	625					630					635					

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GTG	TTC	AAT	AAT	TCG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC	2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	
640					645					650					655	
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC	2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	
				660					665					670		
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG	2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val	
			675					680					685			
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG	2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu	
		690					695					700				
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG	2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	
	705					710					715					
AAG	AAC	ATC	CGC	AGC	AAC	TAT	CCC	GAC	ATG	CAC	AGC	TAC	ATG	GTG	CGC	2689
Lys	Asn	Ile	Arg	Ser	Asn	Tyr	Pro	Asp	Met	His	Ser	Tyr	Met	Val	Arg	
					725					730					735	
TAC	AAC	CAG	CCC	CGC	GTA	GAG	GAA	GCG	CTC	ACT	CAG	CTC	AAG	GCA	GGG	2737
Tyr	Asn	Gln	Pro	Arg	Val	Glu	Glu	Ala	Leu	Thr	Gln	Leu	Lys	Ala	Gly	
				740					745					750		
AAG	CTG	GAC	GCC	TTC	ATC	TAC	GAT	GCT	GCA	GTG	CTC	AAT	TAC	ATG	GCC	2785
Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala	
			755					760					765			
CGC	AAG	GAC	GAG	GGC	TGC	AAG	CTT	GTC	ACC	ATC	GGC	TCC	GGC	AAG	GTC	2833
Arg	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	
		770					775					780				
TTC	GCC	ACG	ACA	GGC	TAT	GGC	ATC	GCC	CTG	CAC	AAG	GGC	TCC	CGC	TGG	2881
Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	His	Lys	Gly	Ser	Arg	Trp	
	785					790					795					
AAG	CGG	CCC	ATC	GAC	CTG	GCG	TTG	CTG	CAG	TTC	CTG	GGG	GAT	GAT	GAG	2929
Lys	Arg	Pro	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Asp	Glu	
	800				805					810					815	
ATC	GAG	ATG	CTG	GAG	CGG	CTG	TGG	CTC	TCT	GGG	ATC	TGC	CAC	AAT	GAC	2977
Ile	Glu	Met	Leu	Glu	Arg	Leu	Trp	Leu	Ser	Gly	Ile	Cys	His	Asn	Asp	
				820					825					830		
AAA	ATC	GAG	GTG	ATG	AGC	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GCG	GGC	3025
Lys	Ile	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Ala	Gly	
			835					840					845			
GTC	TTC	TAC	ATG	CTC	CTG	GTG	GCC	ATG	GGC	CTG	TCC	CTG	CTG	GTC	TTC	3073
Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ser		Leu	Val	Phe	
		850					855					860				
GCC	TGG	GAG	CAC	CTG	GTG	TAC	TGG	CGC	CTG	CGG	CAC	TGC	CTG	GGG	CCC	3121
Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Arg	Leu	Arg	His	Cys	Leu	Gly	Pro	
	865					870					875					
ACC	CAC	CGC	ATG	GAC	TTC	CTG	CTG	GCC	TTC	TCC	AGG	GGC	ATG	TAC	AGC	3169
Thr	His	Arg	Met	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Met	Tyr	Ser	
				885						890					895	
TGC	TGC	AGC	GCT	GAG	GCC	GCC	CCA	CCG	CCC	GCC	AAG	CCC	CCG	CCG	CCG	3217
Cys	Cys	Ser	Ala	Glu	Ala	Ala	Pro	Pro	Pro	Ala	Lys	Pro	Pro	Pro	Pro	
				900					905					910		

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CCA Pro	CAG Gln	CCC Pro	CTG Leu 915	CCC Pro	AGC Ser	CCC Pro	GCG Ala	TAC Tyr 920	CCC Pro	GCG Ala	CCG Pro	GGG Gly 925	CCG Pro	GCT Ala	CCC Pro	3265
GGG Gly	CCC Pro	GCA Ala 930	CCT Pro	TTC Phe	GTC Val	CCC Pro	CGC Arg 935	GAG Glu	CGC Arg	GCC Ala	TCA Ser	GTG Val 940	GCC Ala	CGC Arg	TGG Trp	3313
CGC Arg	CGG Arg 945	CCC Pro	AAG Lys	GGC Gly	GCG Ala	GGG Gly 950	CCG Pro	CCG Pro	GGG Gly	GGC Gly	GCG Ala 955	GGC Gly	CTG Leu	GCC Ala	GAC Asp	3361
GGC Gly 960	TTC Phe	CAC His	CGC Arg	TAC Tyr 965	TAC Tyr	GGC Gly	CCC Pro	ATC Ile	GAG Glu	CCG Pro 970	CAG Gln	GGC Gly	CTA Leu	GGC Gly	CTC Leu 975	3409
GGC Gly	CTG Leu	GGC Gly	GAA Glu 980	GCG Ala	CGC Arg	GCG Ala	GCA Ala	CCG Pro	CGG Arg 985	GGC Gly	GCA Ala	GCC Ala	GGG Gly	CGC Arg 990	CCG Pro	3457
CTG Leu	TCC Ser	CCG Pro 995	CCG Pro	GCC Ala	GCT Ala	CAG Gln	CCC Pro	CCG Pro 1000	CAG Gln	AAG Lys	CCG Pro	CCG Pro	GCC Ala 1005	TCC Ser	TAT Tyr	3505
TTC Phe	GCC Ala 1010	ATC Ile	GTA Val	CGC Arg	GAC Asp	AAG Lys	GAG Glu 1015	CCA Pro	GCC Ala	GAG Glu	CCC Pro	CCC Pro	GCC Ala	GGC Gly	GCC Ala	3553
TTC Phe	CCC Pro 1025	GGC Gly	TTC Phe	CCG Pro	TCC Ser	CCG Pro 1030	CCC Pro	GCG Ala	CCC Pro	CCC Pro	GCC Ala 1035	GCC Ala	GCG Ala	GCC Ala	ACC Thr	3601
GCC Ala 1040	GTC Val	GGG Gly	CCG Pro	CCA Pro	CTC Leu 1045	TGC Cys	CGC Arg	TTG Leu	GCC Ala	TTC Phe 1050	GAG Glu	GAC Asp	GAG Glu	AGC Ser	CCG Pro 1055	3649
CCG Pro	GCG Ala	CCC Pro	GCG Ala	CGG Arg 1060	TGG Trp	CCG Pro	CGC Arg	TCG Ser	GAC Asp 1065	CCC Pro	GAG Glu	AGC Ser	CAA Gln	CCC Pro 1070	CTG Leu	3697
CTG Leu	GGG Gly	CCA Pro 1075	GGC Ala	GCG Gly	GGC Gly	GCG Ala	GGG Gly 1080	GGC Gly	ACG Thr	GGG Gly	GGC Gly	GCA Ala 1085	GGC Gly	GGA Gly		3745
GGA Gly	GCC Ala	CCG Pro 1090	GCC Ala	GCT Ala	CCG Pro	CCC Pro	CCG Pro 1095	TGC Cys	TTC Phe	GCC Ala	GCG Ala	CCG Pro 1100	CCC Pro	CCG Pro	TGC Cys	3793
TTT Phe 1105	TAC Tyr	CTC Leu	GAT Asp	GTC Val	GAC Asp	CAG Gln 1110	TCG Ser	CCG Pro	TCG Ser	GAC Asp	TCG Ser 1115	GAG Glu	GAC Asp	TCG Ser	GAG Glu	3841
AGC Ser 1120	CTG Leu	GCC Ala	GGC Gly	GCG Ala	TCC Ser 1125	CTG Leu	GCC Ala	GGC Gly	CTG Leu	GAT Asp 1130	CCC Pro	TGG Trp	TGG Trp	TTC Phe	GCC Ala 1135	3889
GAC Asp	TTC Phe	CCT Pro	TAC Tyr 1140	CCG Pro	TAT Tyr	GCC Ala	GAT Asp	CGC Arg	CTC Leu 1145	GGG Gly	CSG Xaa	CCC Pro	GCG Ala	GCA Ala 1150	CGC Arg	3937
TAC Tyr	GGA Gly	TTG Leu	GTC Val 1155	GAC Asp	AAA Lys	CTA Leu	GGG Gly	GGC Gly	TGG Trp 1160	CTC Leu	GCC Ala	GGG Gly	AGC Ser 1165	TGG Trp	GAC Asp	3985
TAC Tyr	CTG Leu	CCT Pro 1170	CCS Xaa	CGC Arg	AGC Ser	GGT Gly	CGG Arg 1175	GCC Ala	GCC Ala	TGG Trp	CAC His	TGT Cys 1180	CGG Arg	CAC His	TGC Cys	4033

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GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCG CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273
CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro 1265 1270 1275	4321
CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg 1280 1285 1290 1295	4369
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCG CTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser 1300 1305 1310	4417
CAC CGG AGA CAC CGG GGC GGG GAC CTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala 1315 1320 1325	4465
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCGGCC CCGGGGGCCC His Phe Ser Ser Leu Glu Ser Glu Val 1330 1335	4512
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGGAAGGAAA GCAGTGGAAC TGGCCGGACC CCGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met 1 5 10 15
Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala 20 25 30
Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly Ala

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35					40					45					
Arg	Pro	Leu	Asn	Val	Ala	Leu	Val	Phe	Ser	Gly	Pro	Ala	Tyr	Ala	Ala
	50					55					60				
Glu	Ala	Ala	Arg	Leu	Gly	Pro	Ala	Val	Ala	Ala	Ala	Val	Arg	Ser	Pro
	65					70					75				80
Gly	Leu	Asp	Val	Arg	Pro	Val	Ala	Leu	Val	Leu	Asn	Gly	Ser	Asp	Pro
				85					90					95	
Arg	Ser	Leu	Val	Leu	Gln	Leu	Cys	Asp	Leu	Leu	Ser	Gly	Leu	Arg	Val
			100					105					110		
His	Gly	Val	Val	Phe	Glu	Asp	Asp	Ser	Arg	Ala	Pro	Ala	Val	Ala	Pro
		115					120					125			
Ile	Leu	Asp	Phe	Leu	Ser	Ala	Gln	Thr	Ser	Leu	Pro	Ile	Val	Ser	Glu
	130					135					140				
His	Gly	Gly	Ala	Ala	Leu	Val	Leu	Thr	Pro	Lys	Glu	Lys	Gly	Ser	Thr
	145					150					155				160
Phe	Leu	His	Leu	Gly	Ser	Ser	Pro	Glu	Gln	Gln	Leu	Gln	Val	Ile	Phe
				165					170					175	
Glu	Val	Leu	Glu	Glu	Tyr	Asp	Trp	Thr	Ser	Phe	Val	Ala	Val	Thr	Thr
			180					185					190		
Arg	Ala	Pro	Gly	His	Arg	Ala	Phe	Leu	Ser	Tyr	Ile	Glu	Val	Leu	Thr
		195					200					205			
Asp	Gly	Ser	Leu	Val	Gly	Trp	Glu	His	Arg	Gly	Ala	Leu	Thr	Leu	Asp
	210					215					220				
Pro	Gly	Ala	Gly	Glu	Ala	Val	Leu	Ser	Ala	Gln	Leu	Arg	Ser	Val	Ser
	225					230					235				240
Ala	Gln	Ile	Arg	Leu	Leu	Phe	Cys	Ala	Arg	Glu	Glu	Ala	Glu	Pro	Val
				245					250					255	
Phe	Arg	Ala	Ala	Glu	Glu	Ala	Gly	Leu	Thr	Gly	Ser	Gly	Tyr	Val	Trp
			260					265					270		
Phe	Met	Val	Gly	Pro	Gln	Leu	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Ala	Pro
		275					280					285			
Gly	Glu	Pro	Pro	Leu	Leu	Pro	Gly	Gly	Ala	Pro	Leu	Pro	Ala	Gly	Leu
	290					295					300				
Phe	Ala	Val	Arg	Ser	Ala	Gly	Trp	Arg	Asp	Asp	Leu	Ala	Arg	Arg	Val
	305					310					315				320
Ala	Ala	Gly	Val	Ala	Val	Val	Ala	Arg	Gly	Ala	Gln	Ala	Leu	Leu	Arg
				325					330				335		
Asp	Tyr	Gly	Phe	Leu	Pro	Glu	Leu	Gly	His	Asp	Cys	Arg	Ala	Gln	Asn
			340					345					350		
Arg	Thr	His	Arg	Gly	Glu	Ser	Leu	His	Arg	Tyr	Phe	Met	Asn	Ile	Thr
		355					360					365			
Trp	Asp	Asn	Arg	Asp	Tyr	Ser	Phe	Asn	Glu	Asp	Gly	Phe	Leu	Val	Asn
	370					375					380				
Pro	Ser	Leu	Val	Val	Ile	Ser	Leu	Thr	Arg	Asp	Arg	Thr	Trp	Glu	Val
	385					390					395				400



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Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp  
 405 410 415  
 Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu  
 420 425 430  
 Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala  
 435 440 445  
 Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser  
 450 455 460  
 Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu  
 465 470 475 480  
 Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala  
 485 490 495  
 His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys  
 500 505 510  
 His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val  
 515 520 525  
 Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu  
 530 535 540  
 Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly  
 545 550 555 560  
 Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala  
 565 570 575  
 Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met  
 580 585 590  
 Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser  
 595 600 605  
 Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly  
 610 615 620  
 Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val  
 625 630 635 640  
 Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys  
 645 650 655  
 Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser  
 660 665 670  
 Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp  
 675 680 685  
 Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln  
 690 695 700  
 Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys  
 705 710 715 720  
 Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr  
 725 730 735  
 Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys  
 740 745 750  
 Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg

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755					760					765					
Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val	Phe
770					775					780					
Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	His	Lys	Gly	Ser	Arg	Trp	Lys
785					790					795					800
Arg	Pro	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Asp	Glu	Ile
				805					810					815	
Glu	Met	Leu	Glu	Arg	Leu	Trp	Leu	Ser	Gly	Ile	Cys	His	Asn	Asp	Lys
			820					825					830		
Ile	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Ala	Gly	Val
		835					840					845			
Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ser	Leu	Leu	Val	Phe	Ala
	850					855					860				
Trp	Glu	His	Leu	Val	Tyr	Trp	Arg	Leu	Arg	His	Cys	Leu	Gly	Pro	Thr
865					870					875					880
His	Arg	Met	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Met	Tyr	Ser	Cys
				885					890					895	
Cys	Ser	Ala	Glu	Ala	Ala	Pro	Pro	Pro	Ala	Lys	Pro	Pro	Pro	Pro	Pro
			900					905					910		
Gln	Pro	Leu	Pro	Ser	Pro	Ala	Tyr	Pro	Ala	Pro	Gly	Pro	Ala	Pro	Gly
		915				920						925			
Pro	Ala	Pro	Phe	Val	Pro	Arg	Glu	Arg	Ala	Ser	Val	Ala	Arg	Trp	Arg
	930					935					940				
Arg	Pro	Lys	Gly	Ala	Gly	Pro	Pro	Gly	Gly	Ala	Gly	Leu	Ala	Asp	Gly
945					950					955					960
Phe	His	Arg	Tyr	Tyr	Gly	Pro	Ile	Glu	Pro	Gln	Gly	Leu	Gly	Leu	Gly
				965					970					975	
Leu	Gly	Glu	Ala	Arg	Ala	Ala	Pro	Arg	Gly	Ala	Ala	Gly	Arg	Pro	Leu
			980					985					990		
Ser	Pro	Pro	Ala	Ala	Gln	Pro	Pro	Gln	Lys	Pro	Pro	Ala	Ser	Tyr	Phe
		995					1000					1005			
Ala	Ile	Val	Arg	Asp	Lys	Glu	Pro	Ala	Glu	Pro	Pro	Ala	Gly	Ala	Phe
	1010					1015						1020			
Pro	Gly	Phe	Pro	Ser	Pro	Pro	Ala	Pro	Pro	Ala	Ala	Ala	Ala	Thr	Ala
1025					1030					1035					1040
Val	Gly	Pro	Pro	Leu	Cys	Arg	Leu	Ala	Phe	Glu	Asp	Glu	Ser	Pro	Pro
				1045					1050					1055	
Ala	Pro	Ala	Arg	Trp	Pro	Arg	Ser	Asp	Pro	Glu	Ser	Gln	Pro	Leu	Leu
			1060					1065					1070		
Gly	Pro	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Thr	Gly	Gly	Ala	Gly	Gly	Gly
		1075					1080					1085			
Ala	Pro	Ala	Ala	Pro	Pro	Pro	Cys	Phe	Ala	Ala	Pro	Pro	Pro	Cys	Phe
	1090					1095					1100				
Tyr	Leu	Asp	Val	Asp	Gln	Ser	Pro	Ser	Asp	Ser	Glu	Asp	Ser	Glu	Ser
1105					1110					1115				1120	

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Leu	Ala	Gly	Ala	Ser	Leu	Ala	Gly	Leu	Asp	Pro	Trp	Trp	Phe	Ala	Asp
				1125								1135			
Phe	Pro	Tyr	Pro	Tyr	Ala	Asp	Arg	Leu	Gly	Xaa	Pro	Ala	Ala	Arg	Tyr
				1140								1150			
Gly	Leu	Val	Asp	Lys	Leu	Gly	Gly	Trp	Leu	Ala	Gly	Ser	Trp	Asp	Tyr
				1155								1165			
Leu	Pro	Xaa	Arg	Ser	Gly	Arg	Ala	Ala	Trp	His	Cys	Arg	His	Cys	Ala
				1170								1180			
Ser	Leu	Glu	Leu	Leu	Pro	Pro	Pro	Arg	His	Leu	Ser	Cys	Ser	His	Asp
				1185								1195			
Gly	Leu	Asp	Gly	Gly	Trp	Trp	Ala	Pro	Pro	Pro	Pro	Pro	Trp	Ala	Ala
				1205								1215			
Gly	Pro	Leu	Pro	Arg	Arg	Arg	Ala	Arg	Cys	Gly	Cys	Pro	Arg	Ser	His
				1220								1230			
Pro	His	Arg	Pro	Arg	Ala	Ser	His	Arg	Thr	Pro	Ala	Ala	Ala	Ala	Pro
				1235								1245			
His	His	His	Arg	His	Arg	Arg	Ala	Ala	Gly	Gly	Trp	Asp	Leu	Pro	Pro
				1250								1260			
Pro	Ala	Pro	Thr	Ser	Arg	Ser	Leu	Glu	Asp	Leu	Ser	Ser	Cys	Pro	Arg
				1265								1275			
Ala	Ala	Pro	Ala	Arg	Arg	Leu	Thr	Gly	Pro	Ser	Arg	His	Ala	Arg	Arg
				1285								1295			
Cys	Pro	His	Ala	Ala	His	Trp	Gly	Pro	Pro	Leu	Pro	Thr	Ala	Ser	His
				1300								1310			
Arg	Arg	His	Arg	Gly	Gly	Asp	Leu	Gly	Thr	Arg	Arg	Gly	Ser	Ala	His
				1315								1325			
Phe	Ser	Ser	Leu	Glu	Ser	Glu	Val								
				1330								1335			

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCCT ACTCCAAGAT CTGGCCCTAG  
TCCATGTTTG C

60

71

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGGTGGTCCC CAACCTGTAG GACTTGGTTC TGGAGGAGGA TCTGGTGTAG GCAAACATGG	60
ACTAGGGCCA G	71

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG	60
G	61

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGTGAGACGT CAGACAAAGG AGGCCCAGGT GTAGGTGGTC TACCAGGTGG TTGTGGAGCT	60
CT	62

(2) INFORMATION FOR SEQ ID NO:63:

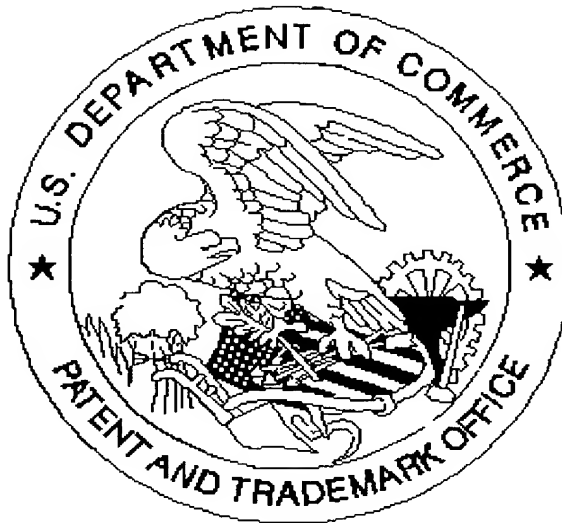
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCGCAGAGCA CCTCCACCAT CTCCTTGTC TACTCCAAGA TCTGGCCCTA GTCCATGTTT	60
GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACCAC CAGATGGAGG	120
TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC	180
TCCTTTGTCT GACGT	195

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☐ *Scanned copy is best available. Sequence listing on page  
68 to 164 in specification*